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Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure underpinning obesity

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ABSTRACT

Genome-wide association studies (GWAS) have identified >250 loci for body mass index (BMI), implicating pathways related to neuronal biology. Most GWAS loci represent clusters of common, non-coding variants from which pinpointing causal genes remains challenging. Here, we combined data from 718,734 individuals to discover rare and low-frequency (MAF<5%) coding variants associated with BMI. We identified 14 coding variants in 13 genes, of which eight in genes (*ZBTB7B, ACHE, RAPGEF3, RAB21*, *ZFHX3*, *ENTPD6, ZFR2, ZNF169*) newly implicated in human obesity, two (*MC4R, KSR2*) previously observed in extreme obesity, and two variants in *GIPR*. Effect sizes of rare variants are ~10 times larger than of common variants, with the largest effect observed in carriers of an *MC4R* stop-codon (p.Tyr35Ter, MAF=0.01%), weighing ~7kg more than non-carriers. Pathway analyses confirmed enrichment of neuronal genes and provide new evidence for adipocyte and energy expenditure biology, widening the potential of genetically-supported therapeutic targets to treat obesity.

Obesity is a heritable disease and represents a major unmet public health problem with only a few safe and long-term effective therapies[1] and intervention strategies[2]. To understand the genetic basis of obesity and identify potential targets for new therapies, genome-wide association studies (GWAS) for body mass index (BMI) and obesity risk have identified >250 common variants over the past decade[3-7]. Consistent with single-gene disorders of obesity[8], tissue expression and gene-set enrichment analyses for genes in BMI-associated loci have shown that the central nervous system (CNS) plays a critical role in body weight regulation[5]. While the numerous GWAS loci have provided insight into broad biological mechanisms underlying body weight regulation, pinpointing the causal gene(s)/variant(s) remains a major challenge[9], as GWAS-identified variants are typically non-coding and may affect genes at long distance. The association of intronic *FTO* variants with BMI illustrates the challenges of identifying causal regulatory effects. The proposed causal variant was found to regulate the expression of nearby *RPGRIP1L* in some studies[10-12], whereas others found that it regulates distant *IRX3/IRX5* genes in specific cell types[13,14].

To expedite mapping of obesity-related genes, we performed an exome-wide search for low-frequency (LF, minor allele frequency [MAF]=1-5%) and rare (R, MAF<1%) single nucleotide variants (SNVs) associated with BMI using exome-targeted genotyping arrays. A total of 125 studies ($N_{individuals}$=718,734) performed single-variant association between up to 246,328 SNVs and BMI. In addition, we performed gene-based meta-analyses to aggregate rare and LF (R/LF) coding SNVs across 14,541 genes. Using genetic, functional and computational follow-up analyses, we gained insights into the function of BMI-implicated genes, and the biological pathways through which they may influence body weight.

RESULTS

Fourteen rare and low-frequency coding variants in 13 genes

Our study comprises a discovery and a follow-up stage (**Supplementary Figure 1**, **Supplementary Tables 1-3, Online Methods**). In our primary analysis, the discovery stage includes data from 123 studies (N_{max}=526,508) across five ancestry groups, predominantly European (~85%). Each study performed

single-variant association analyses of coding variants present on the exome array, including up to 13,786 common (MAF>5%) and 215,917 R/LF coding SNVs (exons and splicing sites). Summary statistics were combined using fixed-effect meta-analyses. SNV-associations of R/LF variants that reached suggestive significance ($P<2.0x10^{-6}$) were taken forward for follow-up in two European cohorts, deCODE (N_{max}=72,613) and UK Biobank (N_{max}=119,613 [interim release]). Overall significance was assessed after combining results of discovery and follow-up studies into a final meta-analysis (all-ancestries, sex-combined, additive model, N_{max}=718,734), SNV-associations that reached $P<2x10^{-7}$ were considered array-wide significant[15,16] (**Table 1**, **Supplementary Table 4, Supplementary Figures 2-4**). In secondary analyses, we performed sex-specific analyses, analyses limited to individuals of European ancestry, and analyses using a recessive model.

In our primary analysis of R/LF variants, we identified five rare SNVs in three genes (*KSR2,* 2 in *MC4R,* 2 in *GIPR*) and nine LF SNVs in eight genes (*ZBTB7B, 2 in ACHE, RAPGEF3, PRKAG1, RAB21, HIP1R, ZFHX3, ENTPD6*) (**Table 1**, **Box 1**, **Supplementary Table 5, Supplementary Figure 3a**). In secondary analyses, we identified two additional LF SNVs, one in all-ancestry women-only (*ZFR2*) and one in European ancestry only analyses (*ZNF169*) (**Table 1**, **Supplementary Tables 6-8, Supplementary Figures 3b, 3c**). Of these 16 SNVs, located in 13 genes, the two SNVs in *MC4R* (r^2=1, *D'*=1) and two in *ACHE* (r^2=0.98, *D'*=0.99) were in high LD, whereas the two SNVs in *GIPR* (r^2=0, *D'*=0.16) were independent of each other. Hence, the 16 SNVs represent 14 independent SNVs (4 rare, 10 LF), of which eight locate in genes not previously implicated in BMI (*ZBTB7B, ACHE, RAPGEF3, RAB21, ZFHX3, ENTPD6, ZFR2, ZNF169*), and six are located in five loci that were previously identified by GWAS (*PRKAG1/BCDIN3D, HIP1R/CLIP1, MC4R, GIPR/QPCTL*)[5] and/or through sequencing of severe early-onset obesity cases (*MC4R, KSR2*)[17-19] (**Supplementary Figure 5**). Conditional analyses established that coding SNVs in *PRKAG1, MC4R* and *GIPR* are independent of the common lead variants in GWAS loci (rs7138803, rs17782313, rs2287019, respectively), whereas the SNV in *HIP1R* and GWAS locus near *CLIP1* (rs11057405) represent the same signal (**Online Methods, Supplementary Tables 9, 10, Supplementary Figure 5**).

Next, we performed gene-based association tests (SKAT, VT, broad, strict) in up to 14,541 genes[20] to examine whether these aggregated analyses would yield new evidence for multiple R/LF coding SNVs in the same gene affecting BMI (**Online Methods**). Using broad SNV inclusion criteria, associations for 13 genes reached array-wide significance ($P<2.5x10^{-6}$)[15,16], four of which had not been highlighted in single-variant analyses (**Table 2, Supplementary Table 11**). Conditional analyses showed that only for *GIPR* was the gene-based association driven by multiple SNVs (**Table 2**, **Supplementary Table 12**). For all other genes, associations were driven by a single SNV only, but these SNVs had not reached array-wide significance in single-variant analyses.

Taken together, we identified 14 R/LF coding SNVs in 13 genes that are independently associated with BMI, four rare SNVs in three genes, and 10 LF SNVs in 10 genes. One SNV (*ZFR2*) showed a sex-specific effect, whereas no ancestry-specific effects were observed (**Supplementary Note**, **Supplementary Tables 6-8**, **Supplementary Figure 6**). Eight (*ACHE*, *ENTPD6*, *RAB21*, *RAPGEF3*, *ZBTB7B*, *ZFHX3*, *ZFR2*, *ZNF169*) of these 13 genes have not been previously implicated in body weight regulation (**Table 1**).

Novel common coding variants associated with BMI

Although the main focus of our study was on R/LF coding SNVs, we also identified 92 common coding variants ($P<2.0x10^{-7}$, **Supplementary Tables 4, Supplementary Figures 4, 7**), of which 41 were novel (**Supplementary Table 9, Supplementary Note**). These novel common loci had not been identified in previous GWAS efforts, because our current sample size is more than twice as large as the most recent GWAS meta-analysis[5], and also because some SNVs were not tested before, as they were not present on the HapMap reference panel and/or were on the X-chromosome, which was not analyzed. Because of the increased samples size, effect sizes of the 41 novel common loci are smaller (on average 0.014 SD/allele, [range: 0.010–0.024]) than of previously established common loci (0.021 SD/allele, [0.010–0.050]) (**Supplementary Figure 7**).

Impact of R/LF SNVs on BMI and obesity risk

The minor allele for half of the 14 R/LF SNVs is associated with lower BMI (**Table 1, Figure 1**). The effects of LF SNVs range between 0.024 and 0.066 SD/allele, equivalent to ~0.11 to 0.30 kg/m^2 in BMI or ~0.315 to 0.864 kg in body weight for a 1.7m tall person. Effects of rare SNVs range between 0.06 and 0.54 SD per allele, equivalent to 0.26 to 2.44 kg/m^2 or 0.74 kg to 7.05 kg per allele (**Table 1, Figure 1**). By comparison, these rare SNV effect sizes are on average ten times larger than those for previously identified GWAS loci (effect$_{mean}$=0.019 SD/allele, ~0.086 kg/m^2 or ~0.247 kg/allele) of which the largest effect is seen for the *FTO* locus (0.08 SD/allele, ~0.35 kg/m^2 or 1 kg/allele) and those for other GWAS loci range between 0.010 and 0.056 SD/allele (~0.045 to 0.25 kg/m^2, or 0.130 to 0.728 kg)[5].

Effect sizes increase as MAF decreases, in particular for SNVs with a MAF<0.5% (~1 heterozygote carrier in 100 people), consistent with the statistical power of our sample (**Figure 1**). For example, the nonsense p.Tyr35Ter *MC4R* SNV (rs13447324, MAF=0.01%) is present in ~1 in 5,000 individuals and results in a ~7 kg higher body weight for a 1.7m tall person. The two *GIPR* SNVs contribute independently to a *lower* body weight, carriers (1 in ~455 individuals) of p.Arg190Gln (rs139215588) weigh ~1.92 kg (0.148 SD BMI) less than non-carriers and carriers (1 in ~385 individuals) of p.Glu288Gly (rs143430880) weigh ~1.99 kg (0.153 SD BMI) less. Among 115,611 individuals of the UK Biobank, one apparently healthy 61-year-old woman, with no reported illnesses, carried both rare *GIPR* alleles and weighed ~11.2 kg less (equivalent to -0.86 SD BMI or 3.87 kg/m^2) than the average non-carrier of the same height (**Supplementary Figure 8)**. The possible synergistic effect of the two *GIPR* alleles needs confirmation by additional individuals that carry both variants.

Even though effect sizes of LF and, in particular, rare SNVs tend to be larger than those of common GWAS-identified loci[5], the 14 SNVs combined explain <0.1% of BMI variation, because of their low population frequency (**Table 1**, **Online Methods**). Also, although the effects of the four rare SNVs (*KSR2*, *MC4R*, 2 in *GIPR*) are large by GWAS standards, penetrance for obesity is still expected to be low. Indeed, using data from the UK Biobank (N$_{max}$=119,781), we compared the prevalence of normal-weight (18.5 kg/m^2 ≤ BMI < 25 kg/m^2) and obesity (BMI ≥ 30 kg/m^2) between carriers and non-carriers (**Supplementary Table 13**, **Online Methods**). For *GIPR* (p.Arg190Gln, p.Glu288Gly), both BMI-decreasing SNVs, carriers

tended (P<0.05) to have a lower obesity prevalence (21.2%, 20.1%, respectively), compared to non-carriers (25.1%, 25%). For *MC4R* p.Tyr35Ter and *KSR2* p.Arg525Gln, the prevalence of obesity between carriers (30%, 25.7%, resp.) and non-carriers (25.1%, 25.3%) was not significantly different.

We examined whether R/LF SNVs affect obesity risk early on in life by combining data from three case-controls studies of childhood obesity (N_{cases}=4,395, $N_{controls}$=13,072) (**Online Methods, Supplementary Table 14**). Associations for 10 of 13 SNVs were directionally consistent with those observed for BMI in adults (77%, $P_{binomial}$=0.046), three of which (*ZBTB7B*, *PRKAG1*, *RAB21*) reached nominal significance (P<0.05). While no carriers of the *MC4R* mutations were available for analyses, the role of *MC4R* in body weight regulation in childhood was established almost two decades ago[17,19,21].

Impact of R/LF SNVs on cardiometabolic and other traits

To examine whether identified SNVs affect other traits, we obtained results from multiple large-scale genetic consortia (GIANT[15], MAGIC, GoT2D/T2D-GENES[16], GLGC, ICBP[22], REPROGEN[23]) (**Supplementary Table 15, Supplementary Figure 9)**, and performed phenome-wide association (PheWAS) analyses using electronic medical record (EMR) data from BioVu and UK Biobank (**Online Methods**, **Supplementary Table 16**). The BMI-increasing allele of *ZBTB7B* p.Pro190Ser is associated with greater height, and those of *PRKAG1*, *ACHE*, and *RAPGEF3* SNVs are associated with shorter height, but association with other traits differ. Specifically, *PRKAG1* p.Thr38Ser Ser-allele carriers appear heavier and shorter, have lower HDL-cholesterol levels, earlier age at menarche (reported before[23]) and higher systolic blood pressure, which is in agreement with PheWAS analyses showing an increased risk of "malignant essential hypertension" and "hypertension" (**Supplementary Table 16**). While carriers of the *RAPGEF3* p.Leu300Pro Pro-allele are also heavier and shorter, they have a lower WHR_{adjBMI}[24] and lower fasting insulin levels (**Supplementary Table 15),** consistent with PheWAS results that show lower odds of "secondary diabetes mellitus" (**Supplementary Table 16**). Thus, while all SNVs are associated with BMI, their patterns of association with other traits suggest they may affect different physiological pathways.

Gene set enrichment analyses

To test whether the R/LF variants implicate biological pathways, we performed gene set enrichment analyses. Similar to our previous analysis of GWAS for BMI[5], we analyzed coding variants that reached $P<5x10^{-4}$, using a DEPICT version adapted for exome-array analysis[15] (**Online Methods, Supplementary Note**). We used 50 R/LF coding variants as input (all $P<5x10^{-4}$, **Online Methods**) and observed significant enrichment (**Figure 2, Supplementary Table 17, Supplementary Figure 10a**). Many of these relate to neuronal processes, such as neurotransmitter release and synaptic function (e.g. glutamate receptor activity, regulation of neurotransmitter levels, synapse part), consistent with previous findings from GWAS[5]. When we excluded variants near (+/- 1Mb) previously identified GWAS loci, we still observed 29 significantly enriched gene sets (in 12 meta-gene sets) (**Supplementary Table 18, Supplementary Figure 10b**), thereby providing an independent confirmation of the GWAS gene set enrichment results. In addition to neuronal-related gene sets, the analyses with R/LF coding variants newly identified a cluster of metabolic pathways related to insulin action and adipocyte/lipid metabolism (e.g. enhanced lipolysis, abnormal lipid homeostasis, increased circulating insulin level, **Figure 2**). Finally, we observed that R/LF BMI-associated coding variants are more effective at identifying enriched gene sets compared to common coding variants. Specifically, adding 192 common coding SNVs (all $P<5x10^{-4}$) to the analysis decreased the number of enriched gene sets from 471 (106 meta-gene sets) seen with R/LF coding SNVs to 62 (24 meta-gene sets) (**Supplementary Table 19, Supplementary Figure 10c**). We observed fewer significant genes sets with the combined common and R/LF analysis, despite including more total coding variants and a higher fraction of array-wide significant coding variants. One possible explanation is that R/LF coding variants may fall in the causal gene more often than do common coding variants, which suggests that the R/LF variants are more likely to be causal, rather than simply in LD with causal variants.

We also used gene set enrichment analysis to prioritize candidate genes. Among the genes with R/LF coding variants associated with BMI at $P<5x10^{-4}$, a subset is prominently represented in the CNS-related enriched gene sets (**Figure 2**) and is proposed to influence neurotransmission and/or synaptic organization, function and plasticity. These include genes in regions with suggestive evidence of association from GWAS (e.g. *CARTPT, MAP1A, ERC2*) and genes in regions not previously implicated by GWAS

(e.g. *CALY, ACHE, PTPRD, GRIN2A*). The non-neuronal metabolic gene sets implicate two genes (*CIDEA*, *ADH1B*) that are markers of brown or "beige" adipose tissue[25,26], providing new supporting evidence for a causal role of this aspect of adipocyte biology.

Drosophila fly results

To test for potential adiposity-driving effects of gene regulation, we performed tissue-specific RNAi-knockdown experiments in *Drosophila*. We generated adipose-tissue (cg-Gal4) and neuronal (elav-Gal4) specific RNAi-knockdown crosses for nine of the 13 candidate genes for which fly orthologues exist (**Supplementary Table 20**) and performed whole body triglyceride analysis in young adult male flies. Triglycerides, the major lipid storage form in animals, were chosen as a direct measure of fly adiposity. Both neuronal and fat-body knockdown of *zfh2*, the orthologue of *ZFHX3*, resulted in significantly increased triglyceride levels. Adipose-tissue specific, but not neuronal, knockdown of *epac* (*RAPGEF3*) was lethal. Tissue-specific loss-of-function of the other seven genes tested did not affect triglyceride levels.

R/LF coding SNVs in monogenic and syndromic genes

We identified 39 genes in the literature that have been convincingly implicated in monogenic obesity or syndromes of which obesity is one of the main features (**Supplementary Table 21, 22, Supplementary Figure 11**). Of the 652 R/LF SNVs in these 39 monogenic and/or syndromic genes, five R/LF SNVs were significantly associated with BMI (Bonferroni-corrected *P*-value = 7.7×10^{-5} (=0.05/652)). Beside SNVs in *MC4R* (p.Tyr35Ter, Asp37Val) and *KSR2* (Arg525Gln), already highlighted in the single-variant analyses, we identified an additional SNV in *MC4R* (p.Ile251Leu) and one in *BDNF* (p.Glu6Lys). *MC4R* p.Ile251Leu has been previously shown to protect against obesity[27], whereas *BDNF* p.Glu6Lys, independent of previously GWAS-identified SNVs (r^2=0.01, D'=1.0)[5], has not been implicated in body weight regulation before. We examined whether the 652 R/LF SNVs showed enrichment for association with BMI compared to R/LF coding SNVs in all other genes, but found no evidence to support this.

DISCUSSION

In this meta-analysis of exome-targeted genotyping data, we identified 14 R/LF coding variants in 13 genes associated with BMI. Eight of these genes (*ACHE, ENTPD6, RAB21, RAPGEF3, ZBTB7B, ZFHX3, ZFR2, ZNF169*) have not been previously implicated in human obesity, but evidence from animal studies provides support for a role in energy metabolism for some of these, such as *ACHE*[28,29], *RAPGEF3*[30-33], and *PRKAG1*[34-39]. Others fall into established BMI GWAS loci (*PRKAG1/BCDIN3D, HIP1R/CLIP1, MC4R, GIPR/QPCTL*)[5] and/or were previously implicated in severe early-onset obesity (*MC4R, KSR2*)[17-19] and using this exome-targeted approach, we pinpoint R/LF variants in these loci that play a role in obesity in the general population. Pathway analyses confirm a key role for neuronal processes, and newly implicate adipocyte and energy expenditure biology.

Consistent with other polygenic traits[15,23,40-43], we show that large sample sizes are needed to identify R/LF variants. Observed effect sizes reflect the statistical power of our sample size, and are particularly large for SNVs with a MAF < 0.05%. The existence of rare alleles with larger effects on BMI than have been observed for common alleles might reflect negative or stabilizing selection on the extremes of BMI. However, rare variants with smaller effects almost certainly exist, larger samples will be needed to uncover these. Our study was limited to coding variants on the exome-array, large-scale sequencing studies will be needed to test for variants not covered by exome-arrays.

The strongest association was observed for a stop-codon (p.Tyr35Ter, rs13447324, MAF= 0.01%) in *MC4R*, with carriers weighing on average 7kg more than non-carriers. *MC4R* is widely expressed in the CNS and is an established key player in energy balance regulation[44,45]. Mouse and human studies showed already two decades ago that MC4R-deficiency results in extreme obesity, mainly through increased food intake[46-49]. p.Tyr35Ter, which results in MC4R-deficiency[51], was one of the first *MC4R* mutations discovered in monogenic cases of obesity[17,19], in whom the mutation is >20x more prevalent than in the general population[17,50,52,53]. Here, we show that p.Tyr35Ter plays a role outside the setting of early-onset and extreme obesity. Despite its large effect, penetrance is low, and does not fit the model of a fully penetrant Mendelian variant.

While significant R/LF coding variants are strong candidates for being causal, the strongest implication of causal genes is provided by association with multiple independent coding variants, as we demonstrate for *GIPR*. We identified two rare variants in *GIPR* (p.Arg190Gln, rs139215588, MAF=0.11%, p.Glu288Gly, rs143430880, MAF=0.13%) independently associated with lower BMI, carriers of either variant weigh ~2 kg less than non-carriers. Common variants in/near *GIPR* have been found to associate with lower BMI[55] and delayed glucose and insulin response to an oral glucose challenge[54]. However, the two rare variants influence BMI independently of these common ones and are not associated with type 2 diabetes or glycemic traits tested. Rodent models have provided strong evidence for a role of GIPR in body weight regulation. *Gipr*-deficient mice are protected from diet-induced obesity[56] and have an increased resting metabolic rate[57]. Blocking GIP-signaling using a vaccination approach in mice on a high-fat diet reduces weight gain, mainly through reduced fat accumulation, mediated through increased energy expenditure[58]. Manipulation of incretins (GIP, GLP1) and their receptors has complex effects on obesity and insulin secretion/action that may differ between human and mice[59]. The human genetic data suggest that inhibition of GIPR-signaling might present a therapeutic target for the treatment of obesity[60].

A fourth rare variant, in *KSR2*, (p.Arg525Gln, rs56214831, MAF=0.82%) increases body weight by ~740g/allele. *KSR2* is another gene previously implicated in energy metabolism and obesity[18,61,62]. In a recent study, mutation carriers were hyperphagic, had a reduced basal metabolic rate and severe insulin resistance[18]. Consistent with human data, *Ksr2*$^{-/-}$ mice were obese, hyperphagic, and had a reduced energy expenditure[18,61-63]. KSR2 is almost exclusively expressed in the brain and interacts with multiple proteins[64], including AMP-activated protein kinase (AMPK), a key regulator of energy homeostasis[61,62]. Interestingly, *KSR2* is one of the first genes implicated in severe, early-onset obesity in which mutations not only affect food intake but also basal metabolic rate, and is thought to act via neuronal effects[18] (**Figure 2**).

Despite convincing associations of these four rare variants in *MC4R*, *GIPR* and *KSR2*, their penetrance for obesity is low (**Supplementary Table 13**). This is consistent with the polygenic and multifactorial nature of obesity, where variants across a range of frequencies and effect sizes contribute to the phenotype in any one person. Despite low predictive power, it remains possible that the identities of

particular variants in any one person may contribute to different balances of underlying physiologies and hence, different responses to treatments. This was illustrated in two patients with monogenic obesity due to *POMC* mutations, these patients lack the main activator of MC4R and were effectively treated with an MC4R-agonist[65].

Of the coding variants in newly identified genes, some have well-known connections to obesity. For example, *PRKAG1* encodes the γ1-subunit of AMPK, a critical cellular energy sensor[34]. In the hypothalamus, AMPK integrates hormonal and nutritional signals with neuronal networks to regulate food intake and whole-body energy metabolism[35-37]. Furthermore, hypothalamic AMPK is a key regulator of brown adipose tissue in mice[36,38,39]. The BMI-decreasing allele at the associated *PRKAG1* variant (p.Thr38Ser, rs1126930, MAF=3.22%) has additional beneficial effects on blood pressure, providing additional genetic support for modulation of AMPK as an ongoing therapeutic avenue for treatment.

ACHE, in which p.His353Asn (rs1799805, MAF=3.9%) is associated with increased BMI, is another candidate gene related to neuronal biology, involved in the signaling of acetylcholine at neuromuscular junction and brain cholinergic synapses[67,68]. Inhibitors of ACHE, used to treat moderate-to-severe Alzheimer's Disease[69], results in weight loss in humans and Ache-deficient mice have delayed weight gain[28,29]. However, these may be indirect consequences of adverse gastrointestinal and neuromuscular effects, respectively[28,29,70,71].

Another LF coding variant (p.Leu300Pro, rs145878042, MAF=1.1%) is located in *RAPGEF3*, and has strong effects on multiple other phenotypes. The BMI-increasing 300Pro-allele is associated with shorter height, lower WHR_{adjBMI} and lower insulin levels, suggesting that this variant has multiple physiologic consequences. Data from animal models also suggest complex effects of RAPGEF3 on adipocyte biology, energy balance and glucose metabolism[30-33]. For example, in one study, global deletion of *Rapgef3* in mice on a high-fat diet are resistant to obesity due to reduced food intake and have an increased glucose tolerance[31]. However, in a similar study, *Rapgef3*$^{-/-}$ mice develop severe obesity, increased respiratory exchange ratio and impaired glucose tolerance[33]. Adipose tissue-specific *Rapgef3* knockout mice on a high-fat diet are also more prone to obesity, show increased food intake, reduced energy

expenditure, impaired glucose tolerance, and reduced circulating leptin levels[72]. More research is needed to understand the consequences of *RAPGEF3* manipulation.

The remaining genes with significant associations, *ENTPD6*, *HIP1R*, *RAB21*, *ZFR2*, *ZBTB7*, and *ZFHX3*, have no clear prior evidence for a role in energy homeostasis, and in-depth functional follow up is needed to gain insight in how they affect body weight. Here, we performed gene set enrichment analyses to better understand the biology implicated by our genetic data, and confirm the importance of neuronal processes, in particular synaptic function and neurotransmitter release, providing an independent validation of previous GWAS findings[5]. The combination of gene set enrichment and association analyses of coding variants also enables us to highlight candidate genes that are both within these gene sets and show association with BMI at R/LF coding variants. These include genes reaching array-wide significance (e.g. *ACHE*, *ZFR2*), and others with clear prior evidence for a role in body weight regulation (e.g. *CARTPT*[73]), but that had not been highlighted in our single-variant or gene-based association analyses. Of note, the enrichment signals were stronger with R/LF coding variants only than with *all* coding variants, suggesting that R/LF variants are more likely to be causal and may more often point directly to relevant genes, whereas common coding variants may more often be proxies for common noncoding variants that affect nearby genes.

In addition, our gene set enrichment analyses now provide supporting evidence for a role of non-neuronal mechanisms as well. Specifically, *CIDEA* and *ADH1B* are both strongly predicted to be members of enriched gene sets related to insulin action and adipocyte biology, and both are markers that distinguish brown from white fat depots in mice[25] and humans[26]. CIDEA is predominantly expressed in adipose tissue and known as a key regulator of energy metabolism[25]. *Cidea*-deficient mice are resistance to diet-induced obesity with increased lipolysis and mitochondrial uncoupling[25]. The connection of *ADH1B* to obesity is less clear, but the gene is highly expressed in human adipocytes, has been implicated by gene expression analyses in obesity and insulin resistance, and functions early in a potentially relevant metabolic pathway (retinoid biosynthesis)[25,26,74,75]. Similar pathways were implicated by recent work dissecting the signal near *FTO*[13]. However, because SNV-association signals at *ADH1B* and *CIDEA* did not reache array-wide

significance, additional genetic analysis of their role in obesity would be warranted.

In summary, we performed association analyses between R/LF variants and BMI in >700,000 individuals, and identified 14 variants in 13 genes, in 5 known and 8 novel genes. While each variant contributes little to BMI variation in the general population, they may have substantial impact on body weight at an individual level. Furthermore, prior literature for these genes and unbiased gene set enrichment analysis indicate a strong role for neuronal biology and also provide new support for a causal role of aspects of adipocyte biology. The identified genes provide potential targets that may lead to new and more precise approaches for the treatment of obesity, which has seen minimal innovation in the past 30 years[1].

URLs

CDC 2000 Growth Charts: http://www.cdc.gov/growthcharts/cdc_charts.htm

CHOP cohort: http://www.metabolic-programming.org/obesity/

EC-DEPICT code: https://github.com/RebeccaFine/obesity-ec-depict

ENSEMBL: www.ensembl.org

EasyQC: www.genepi-regensburg.de/easyqc

EasyStrata: www.genepi-regensburg.de/easystrata

ExAC: http://exac.broadinstitute.org/

GCTA: http://cnsgenomics.com/software/gcta/

GTEx: http://www.gtexportal.org/home/

GTOOL: http://www.well.ox.ac.uk/~cfreeman/software/gwas/gtool.html

Impute2: https://mathgen.stats.ox.ac.uk/impute/impute_v2.html

INTERVAL Study: http://www.intervalstudy.org.uk/

PLINK v1.90: https://www.cog-genomics.org/plink2

QCTOOL: http://www.well.ox.ac.uk/~gav/qctool/#overview

RAREMETALWORKER: http://genome.sph.umich.edu/wiki/RAREMETALWORKER

RareMETALS: http://genome.sph.umich.edu/wiki/RareMETALS

RVTEST: https://github.com/zhanxw/rvtests

Shapeit2: https://mathgen.stats.ox.ac.uk/genetics_software/shapeit/shapeit.html

UKHLS: https://www.understandingsociety.ac.uk/

UK10K Obesity Sample Sets - SCOOP: http://www.uk10k.org/studies/obesity.html

1000 Genomes Phase 1: http://www.1000genomes.org/category/phase-1/

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FIGURE LEGENDS

Figure 1. Effect sizes (y-axis) of the 14 BMI-associated R/LF coding variants by their minor allele frequency. Effect sizes are expressed in body weight (kg) per allele, assuming a SD of 4.5 kg and an average-sized person of 1.7m tall. Solid markers indicate that the minor allele is associated with higher BMI, and clear markers indicate that the minor allele is associated with lower BMI. Variants were identified in all-ancestry analyses (light blue diamonds), the European ancestry analyses (dark blue square) and women-only analyses (pink diamond). Effect sizes for previously identified GWAS loci are shown in navy blue diamonds. The dotted line represents 80% power, assuming $\alpha = 2x10^{-7}$ and N= 525,000 (discovery sample size).

Figure 2. Heatmap showing DEPICT gene set enrichment results for suggestive and significant rare and low-frequency coding SNVs. For any given square, the color indicates how strongly the corresponding gene (x-axis) is predicted to belong to the reconstituted gene set (y-axis), based on the gene's Z-score for gene set inclusion in DEPICT's reconstituted gene sets (red indicates a higher, blue a lower Z-score). To visually reduce redundancy and increase clarity, we chose one representative "meta-gene set" for each group of highly correlated gene sets based on affinity propagation clustering (**Online Methods**, **Supplementary Note**). Heatmap intensity and DEPICT *P*-values (**Supplementary Table 17**) correspond to the most significantly enriched gene set within the meta-gene set. Annotations for genes indicate (1) whether it has an OMIM annotation as underlying a monogenic obesity disorder (black/grey), (2) the MAF of the significant ExomeChip (EC) variant (blue), (3) whether the variant's *P*-value reached array-wide significance ($<2x10^{-7}$) or suggestive significance ($<5x10^{-4}$) (purple), (4) whether the variant was novel, overlapping "relaxed" GWAS signals from Locke *et al.*[5] (GWAS $P<5x10^{-4}$), or overlapping "stringent" GWAS hits (GWAS $P<5x10^{-8}$) (pink), and (5) whether the gene was included in the gene set enrichment analysis or excluded by filters (orange/brown) (**Online Methods, Supplementary Note**). Annotations for gene sets indicate if the meta-gene set was significant (green, FDR <0.01, <0.05, or not significant) in the DEPICT analysis of GWAS results[5]. Here, two regions of particularly strong gene set membership are

shown (see full heat map in **Supplementary Figure 10a)**.

TABLES

Table 1 Rare and low-frequency coding variants significantly associated with BMI

Chr:position	Variant	Coding locus	Allele		Amino acid change	EAF (%)	β (SD/allele)	SE	*P*-value	*N*	Explained variance (%)
			Effect	Other							
All-ancestries additive											
1:154987704	rs141845046	*ZBTB7B**	T	C	p.Pro190Ser	2.44%	0.048	0.006	7.73E-18	718,628	0.011%
7:100490797	rs1799805	*ACHE**	T	G	p.His353Asn	3.90%	0.029	0.005	2.82E-10	707,448	0.006%
12:48143315	rs145878042	*RAPGEF3**	G	A	p.Leu300Pro	1.10%	0.066	0.008	1.56E-15	700,852	0.010%
12:49399132	rs1126930	*PRKAG1*	C	G	p.Thr38Ser	3.22%	0.034	0.005	3.98E-12	712,354	0.007%
12:72179446	rs61754230	*RAB21**	T	C	p.Ser224Phe	1.74%	0.040	0.007	1.33E-09	693,373	0.005%
12:117977550	rs56214831	*KSR2*	T	C	p.Arg525Gln	0.82%	0.057	0.010	1.08E-08	655,049	0.005%
12:123345509	rs34149579	*HIP1R*	T	G	p.Cys938Phe	4.54%	-0.032	0.004	2.00E-14	716,253	0.009%
16:72830539	rs62051555	*ZFHX3**	G	C	p.Gln1100His	4.34%	-0.024	0.004	4.01E-08	690,637	0.005%
18:58039478	rs13447324	*MC4R*	T	G	p.Tyr35Ter	0.01%	0.542	0.086	2.26E-10	631,683	0.006%
19:46178020	rs139215588	*GIPR*	A	G	p.Arg190Gln	0.11%	-0.148	0.028	1.25E-07	695,800	0.005%
19:46180976	rs143430880	*GIPR*	G	A	p.Glu288Gly	0.13%	-0.153	0.028	2.96E-08	599,574	0.006%
20:25195509	rs6050446	*ENTPD6**	A	G	p.Lys185Glu	2.71%	-0.034	0.005	2.40E-10	717,084	0.006%
All-ancestries sex-specific additive (women only)											
19:3813906	rs45465594	*ZFR2**	C	A	p.Ile718Met	2.55%	-0.040	0.008	1.94E-07	373,848	0.008%
European Ancestry additive											
9:97062981	rs12236219	*ZNF169**	T	C	p.Arg381Cys	4.23%	-0.029	0.005	8.78E-10	612,396	0.007%

Array-wide significant is defined as $P < 2x10^{-7}$.
Variant positions are reported according to Build 37 and their alleles are coded based on the positive strand.
Alleles (effect/other), effect allele frequency (EAF), beta (b), standard error (SE) and P values are based on the meta-analysis of Discovery Stage (GIANT) and Validations stage (deCODE, UKBiobank) studies. Effect allele is always the minor allele. Effects (b) are expressed in SD, assuming mean=0 and SD=1.

The amino acid change from the most abundant coding transcript is shown in this table (see Supplementary Table 25 for more details on protein annotation based on VEP tool and transcript abundance from GTEx database).
* Novel gene, i.e. not previously implicated in human obesity

Table 2. Genes significantly associated with BMI in a gene-based meta-analyses, aggregating R/LF coding SNVs

Gene	Location longest coding transcript	Test[d]	*N* variants	*P*-value	*Conditioned P*-value[a]	Single variant	
						Top variant	*P*-value
All-ancestries sex-combined							
SLC6A17	chr1:110693132-110744823	SKAT	13	2.73E-07	0.13	rs41313405	4.45E-07
RAPGEF3	chr12:48128453-48152889	SKAT	19	8.91E-15	0.20	rs145878042	5.16E-14
PRKAG1	chr12:49396055-49412629	SKAT	4	2.75E-12	0.53	rs1126930	2.63E-12
RAB21	chr12:72148643-72187256	SKAT	5	4.81E-08	0.27	rs61754230	4.96E-08
KSR2	chr12:117890817-118406028	SKAT	7	7.15E-09	0.19	rs56214831	4.59E-08
MAP1A	chr15:43809806-43823818	SKAT	25	9.42E-07	0.16	rs55707100	1.01E-06
MC4R	chr18:58038564-58040001	VT	4	3.72E-09	0.01	rs13447325	2.97E-11
GIPR	chr19:46171502-46186982	VT	10	8.24E-09	1.12E-04	rs143430880	5.76E-06
All-ancestries sex-specific							
ALDH3A1 (men only)	chr17:19641298-19651746	SKAT	15	3.24E-07	0.003	rs142078447	8.62E-06
ZFR2 (women only)	chr19:3804022-3869027	SKAT	19	1.81E-07	0.82	rs45465594	3.64E-07
European sex-combined							
ACHE	chr7:100487615-100493592	SKAT	6	3.30E-10	0.12	rs386545548	7.22E-10
European sex-specific							
ANGPTL7 (men only)	chr1:11249346-11256038	VT	3	2.50E-06	0.008	rs202182115	2.56E-05
ZNF169 (women only)	chr9:97021548-97064111	SKAT	9	1.89E-07	0.24	rs12236219	1.06E-06

Array-wide significant gene-based association is defined as $P<2.5x10^{-6}$. P-values are based on the meta-analysis of Discovery Stage studies.

Gene-based analyses were performed with SKAT and VT, results shown are from the test (SKAT or VT) for which the significance exceeded $P<2.5x10^{-6}$. Only results using the "broad" SNV inclusion criteria reached array-wide significance.

Transcript positions are reported according to Build 37 for the longest coding transcript supported by RefSeq (as displayed in USCS Genome Browser).

[a]P-value after conditioning on the most significant (top) single variant aggregated in the gene-based test.

BOX 1 – Brief description of the 13 genes (alphabetical) identified

ACHE (acetylcholinesterase). *ACHE* is mainly expressed in brain and muscle[76]. Its encoded protein hydrolyzes acetylcholine (Ach) at brain cholinergic synapses and neuromuscular junctions, and thus terminates signal transmission[67]. Knockout mice showed a reduction in expression of muscarinic Ach receptors in brain regions associated with learning and memory and showed lower ability to initiate the signaling cascade[77]. This gene has fewer missense variants than expected and is highly intolerant to loss of function (LoF) mutations[52].

ENTPD6 (ectonucleoside triphosphate diphosphohydrolase 6). Previously known as *Interleukin 6 Signal Transducer-2*, this gene is similar to E-type nucleotidases that participate in purine and pyrimidine metabolism, calcium ion binding, hydrolase activity, magnesium ion binding and nucleoside-diphosphatase activity[78]. It is widely expressed in many different tissues, in particular in the brain[76].

GIPR (gastric inhibitory polypeptide receptor). *GIPR* encodes a G-protein coupled receptor for gastric inhibitory polypeptide that is secreted by intestinal K-cells after food ingestion[59]. GIPR activation stimulates insulin secretion from pancreatic β-cells and mediates fat deposition by increasing lipoprotein lipase activity, lipogenesis, fatty acid and glucose uptake in adipocytes. GIPR is mostly expressed in EBV-transformed lymphocytes, stomach and visceral adipose tissue[76].

HIP1R (huntingtin interacting protein 1 related). HIP1R is a multi-domain protein that promotes actin binding and cell survival and interacts with CLTB and HIP1 (GeneCards). HIP1 and HIP1R appear to play central roles in clathrin-coated vesicle formation and intracellular membrane trafficking by promoting transient interaction between actin filaments and the endocytic machinery[79,80]. HIP1R is most expressed in the stomach tissue, brain (substantia nigra, spinal cord, hippocampus), and sun-exposed skin [76].

KSR2 (kinase suppressor of ras 2). KSR2 is an intracellular protein that functions as a molecular scaffold to regulate MAP kinases ERK1/2 and determine cell fates. KSR2 also regulates AMPK activity controlling cellular thermogenesis, fat oxidation, and glucose metabolism[18,61,62]. Knockout mouse models and human

mutations have been linked to obesity risk[62]. KSR2 is almost exclusively expressed in the brain. It has fewer missense variants than expected and is highly intolerant to LoF mutations[52].

MC4R (melanocortin 4 receptor). MC4R is a seven-transmembrane G-protein coupled receptor, predominantly expressed in the brain[76]. MC4R has been known to play a key role in body weight regulation for more than 20 years. Activation of MC4R by α-MSH, a POMC-derived peptide, suppresses food intake, MC4R antagonists increase food intake and *MC4R* deficiency in human and rodent models results in hyperphagia and severe and early-onset obesity[81]. More than 150 *MC4R* mutations have been identified in individuals with severe, early-onset obesity[81], many of which lead to a complete or partial loss of function[82,83]. Up to 6% of individuals with severe, early-onset obesity carry pathogenic mutations in *MC4R*, making *MC4R* deficiency the most common form of monogenic obesity[82,84].

PRKAG1 (protein kinase AMP-activated non-catalytic subunit gamma 1). The protein encoded by *PRKAG1* is one of the gamma regulatory subunits of the AMP-activated protein kinase (AMPK), which is an important energy-sensing enzyme that monitors cellular energy status[34]. AMPK and PRKAG1 are ubiquitously expressed[76]. In the hypothalamus, AMPK influences food intake, energy expenditure and glucose homeostasis[36]. Muscle-specific overexpression of AMPK γ1 subunit in mice results in increased food intake, but does not affect body weight, presumably through a compensatory increased energy expenditure[85].

RAB21 (member RAS oncogene family). RAB21 belongs to the Rab family of monomeric GTPases involved in the control of cellular membrane traffic. The encoded protein is widely expressed[76] and plays a role in the targeted trafficking of integrins, and is involved in the regulation of cell adhesion and migration[86]. *RAB21* is thought to be intolerant to LoF mutations[52].

RAPGEF3 (rap guanine nucleotide exchange factor 3, also EPAC1). *RAPGEF3* encodes the exchange protein directly activated by cAMP isoform 1 (EPAC1), one of two cAMP sensors that are involved in numerous intracellular cAMP-mediated functions[87]. EPAC1 is ubiquitously expressed[76], and insights from mouse knockout models suggest a role in energy homeostasis and the development of obesity and diabetes

through the regulation of leptin and insulin signaling[31,87].

ZFR2 (zinc finger RNA binding protein 2). The biological function of the gene product is as yet undetermined. GO annotations related to this gene include *nucleic acid binding*. It may have a role in dendritic branching and axon guidance[88,89]. ZFR2 is predominantly expressed in the brain[76].

ZBTB7B (zinc finger and BTB domain containing 7B, also ThPOK). ZBTB7B is a transcription factor regulating T-cell fate in the thymus, particularly as the master regulator of $CD4^+$ lineage commitment[90]. It is a repressor of type 1 collagen gene expression[91]. This gene is mainly expressed in T-cell lineages, skin and gastrointestinal tissues. *ZBTB7B* is thought to be intolerant to LoF mutations[52].

ZFHX3 (zinc finger homeobox 3). *ZFHX3* encodes a transcription factor with multiple homeodomains and zinc finger motifs and plays a role in cell-cycle, myogenic and neuronal differentiation. This gene is a tumor suppressor[92] that influences circadian rhythms[93,94] and sleep[94]. It may also contribute to the genesis of atrial fibrillation[95]. *ZFHX3* is highly expressed in arterial tissue and also other tissues[76]. The *ZFHX3* gene is highly intolerant to LoF mutations[52].

ZNF169 (zinc finger protein 169). The biological function of the gene product is as yet unclear. GO annotations suggest that *ZNF169* is involved in *nucleic acid binding and transcriptional regulation*. This gene is ubiquitously expressed[76].

More details and references in Supplementary Table 24.

ONLINE METHODS

Study design & participants

The discovery cohort consisted of 123 studies (163 datasets) comprising 526,508 adult (≥18yrs) individuals of the following ancestries (**Supplementary Figure 1**): 1) European (N = 449,889), 2) South Asian (N = 29,398), 3) African (N = 27,610), 4) East Asian (N = 8,839), and 5) Hispanic (N = 10,772). All participating institutions and coordinating centers approved this project and informed consent was obtained from all study participants. Discovery meta-analyses were carried out in each ancestry separately and in the All-ancestries combined group, for both sex-specific and sex-combined analyses. SNVs for which associations reach suggestive significance ($P<2.0x10^{-6}$) in the discovery analyses, were taken forward for follow-up in 192,226 individuals of European ancestry from the UK BioBank and deCODE. Conditional analyses were conducted in the All-ancestries and European descent groups. Study-specific design, sample quality control and descriptive statistics are provided in **Supplementary Tables 1-3**.

Phenotype

Body mass index (BMI: weight [in kilograms] / height [in meters] ^{2}) was corrected for age, age^2 and genomic principal components (PC, derived from GWAS data, the variants with MAF > 1% on ExomeChip, or ancestry informative markers available on the ExomeChip), as well as any additional study-specific covariates (e.g. recruiting center), in a linear regression model. For studies with non-related individuals, residuals were calculated separately by sex, whereas for family-based studies sex was included as a covariate in the model. Additionally, residuals for case/control studies were calculated separately. Finally, residuals were subject to inverse normal transformation[96].

Genotype calling

The majority of studies followed a standardized protocol and performed genotype calling using the designated manufacturer software, which was then followed by zCall[97]. For 10 studies, participating in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium, the raw intensity data for the samples from seven genotyping centers were assembled into a single project for joint

calling[98]. Study-specific quality control (QC) measures of the genotyped variants were implemented before association analysis (**Supplementary Table 2**).

Statistical analyses

Study-level association analyses. Individual cohorts were analyzed separately for each ancestry, in sex-combined and sex-specific groups, with either RAREMETALWORKER (see URL links at the end of the **Online Methods**) or RVTEST[99] (**Supplementary Table 2**), to associate inverse normal transformed BMI with genotype accounting for potential cryptic relatedness (kinship matrix) in a linear mixed model. These software tools are designed to perform score-statistics based rare-variant association analyses, can accommodate both unrelated and related individuals, and provide single-variant results and variance-covariance matrices. The covariance matrix captures linkage disequilibrium (LD) relationships between markers within 1 Mb, which is used for gene-level meta-analyses and conditional analyses[100]. Single-variant analyses were performed for both additive and recessive models.

Centralized quality-control. A centralized quality-control procedure, implemented in EasyQC[101], was applied to individual cohort association summary statistics to identify cohort-specific problems: (1) assessment of possible problems in BMI transformation, (2) comparison of allele frequency alignment against 1000 Genomes Project phase 1 reference data to pinpoint any potential strand issues, and (3) examination of quantile-quantile (QQ) plots per study to identify any problems arising from population stratification, cryptic relatedness and genotype biases.

Meta-analyses. Meta-analyses were carried out by two different analysts at two sites in parallel. We excluded variants with a call rate < 95%, Hardy-Weinberg equilibrium *P*-value < 1×10^{-7}, or large allele frequency deviations from reference populations (> 0.6 for all-ancestry analyses and > 0.3 for ancestry-specific population analyses). Significance for single-variant analyses was defined at the array-wide level (a Bonferroni-corrected threshold of $P < 2\times10^{-7}$ for ~250,000 SNVs). To test for sex-differences of the significant variants ($P < 2\times10^{-7}$), we calculated the *P*-diff for each SNP, which tests for differences between women-specific and men-specific beta estimates using EasyStrata[102]. For gene-based analyses, we applied

the sequence kernel association test (SKAT)[103] and the Variable Threshold (VT)[104] gene-based methods using two different sets of criteria (broad and strict) to select predicted damaging R/LF variants with MAF < 5%, based on coding variant annotation from five prediction algorithms (PolyPhen2 HumDiv and HumVar, LRT, MutationTaster and SIFT)[20]. Our *broad* gene-based tests included nonsense, stop-loss, splice site, and missense variants that are annotated as damaging by at least one algorithm mentioned above. Our *strict* gene-based tests included only nonsense, stop-loss, splice site, and missense variants annotated as damaging by all five algorithms. Statistical significance for gene-based tests was set at a Bonferroni-corrected threshold of $P < 2.5\times10^{-6}$ for about 20,000 genes[16,105]. Singe-variant and gene-based meta-analyses were both performed using RareMETALS R-package[106]. As our secondary analyses are nested and/or highly correlated with our primary analysis, we chose the same, already stringent, Bonferroni-corrected significance threshold for both analyses.

Genomic inflation. Although the overall λ_{GC} value is in the normal range for all coding variants (λ_{GC} = 1.1, **Supplementary Table 23**), we observed a marked genomic inflation of the test statistics even after adequate control for population stratification (linear mixed model) arising from common markers (λ_{GC} = 1.99, **Supplementary Figure 2a** and **Supplementary Table 23**). Such inflation is expected for a highly polygenic trait like BMI, as was previously confirmed for height[15], and is consistent with our very large sample size[5,107]. Furthermore, some of the inflation may be due to the design of the ExomeChip, which besides R/LF coding SNVs also contains (common and non-coding) SNVs that include previously identified GWAS loci for all traits, including for BMI and BMI-related traits, reported in the GWAS catalogue at the time of its design.

After removing established loci (+/- 1Mb), the excess of significant associations is markedly reduced and inflation reduced (**Supplementary Figures 2c and 2d**).

Furthermore, to exclude the possibility that some of the observed associations between BMI and R/LF SNVs could be due to allele calling problems in the smaller studies, we performed a sensitivity meta-analysis with primarily European ancestry studies totaling >5,000 participants. We found very concordant

effect sizes, suggesting that smaller studies do not bias our results (**Supplementary Figure 12**).

Follow-up Analysis. We sought additional evidence for association of the top signals ($P<2.0x10^{-6}$) identified in the discovery meta-analysis using two independent studies from the UK (UK Biobank, interim release, N = 119,613) and Iceland (deCODE, N = 72,613), respectively (**Supplementary Tables 1-3)**. We used the same QC and analytical methodology as described above. We used the inverse-variance weighted fixed effects meta-analysis in METAL[108], to combine the discovery and follow-up association results. Significant associations were defined at $P < 2\times10^{-7}$ in the combined meta-analysis of discovery, UK Biobank and deCODE results.

***Effect of study design*.** To investigate the potential effect of study design of the participating studies, we tested for heterogeneity between population-based, all case-control studies, T2D case-control studies (**Supplementary Table 26**). None of these comparisons showed significant evidence of heterogeneity ($P<7.4x10^{-5}$, correcting for multiple testing).

Conditional analyses. The RareMETALS R-package[106] was used to identify independent BMI associated signals across the all-ancestry meta-analysis results in the discovery phase. RareMETALS performs conditional analyses by using covariance matrices from each individual cohort to distinguish true signals from the shadows of adjacent significant variants in LD. The conditional associations of all the variants within 1Mb of each R/LF coding variant were analyzed to identify [1] nearby secondary signals and [2] to determine independence from nearby non-coding variants or previously identified GWAS loci (previously defined as a window of 1Mb surrounding the lead SNP). Gene-based conditional analyses were also performed in RareMETALS.

Due to the selective coverage of variants on the ExomeChip, we also conducted the respective conditional analyses in the UK Biobank dataset that included 847,441 genome-wide genotyped markers, and 72,355,667 variants imputed against UK10k haplotype reference panel, merged with the 1000 Genomes Phase 3 reference panel. Where available, directly genotyped variants where used for conditional analyses. Otherwise, imputed variants with good imputation quality (IMPUTE2 info score > 0.6) were used. We used

QCTOOL to extract variants of interest from the original imputed data set. Subsequently, GTOOL was used to convert to PLINK format (genotype calling threshold 0.99) and merged with the directly genotyped variants for conditional analyses in PLINK v1.90b3.35 64-bit (25 Mar 2016).

Conversions of effect size and explained variants. We assumed that 1 SD = 4.5 kg/m^2 BMI-units, based on population based data, and 1.7m as the average height of a person to convert effects sizes in SD-units into body weight. The variance explained by each variant was calculated using the effect allele frequency (f) and beta (β) from the meta analyses using the formula[109] of explained variance = $2f(1-f)\beta^2$.

Penetrance analysis. We examined the penetrance for the four rare SNVs, p.Arg525Gln (rs56214831) in *KSR2*, p.Tyr35Ter (rs13447324) in *MC4R*, and p.Arg190Gln (rs139215588) and p.Glu288Gly (rs143430880) in *GIPR* in European ancestry data from the UKBiobank (N up to 120,000). For each variant, we compared the prevalence of underweight (BMI < 18.5 kg/m^2), normal weight (18.5 kg/m^2 ≤ BMI < 25 kg/m^2), overweight (25 kg/m^2 ≤ BMI < 30 kg/m^2) and obesity (BMI ≥ 30 kg/m^2) of non-carriers with non-carriers. We used a Pearson χ^2 test to test for difference between distributions, and a χ^2 for linear trend to test whether distributions of carriers were shifted compared to non-carriers. For p.Arg525Gln in *KSR2* and p.Tyr35Ter in *MC4R*, we hypothesized that obesity prevalence was higher in carriers than in non-carriers, whereas for the two GIPR variants, we hypothesized that the prevalence of normal weight was higher in carriers than non-carriers.

Associations with obesity for the coding rare and low-frequency loci in children. For each of the 14 R/LF SNVs, we tested for association with childhood obesity in the CHOP cohort (Childhood Obesity: Early Programming by Infant Nutrition), the Severe Childhood Onset Obesity Project (SCOOP), the UK Household Longitudinal Study (UKHLS) and INTERVAL Study (INTERVAL). Summary statistics across the studies were combined using a fixed effects inverse-variance meta-analysis with METAL[108].

In the CHOP study, cases (1,358 boys, 1,060 girls) were defined as having a BMI > 95th percentile

at any point in their childhood. Controls (1,412 boys, 1,143 girls) were defined as having < 50th percentile consistently through throughout childhood. The BMI percentiles are based on the CDC 2000 Growth Charts. All children were classified based on their BMI measurements between the ages of 2 and 18. All individuals are of European ancestry and were collected at the Children's Hospital of Philadelphia. Informed consent was obtained from all study participants and study protocols were approved by the local ethics committees. Genotypes were obtained using the HumanHap550v1, HumanHap550v3, and Human610-Quad high-density SNP arrays from Illumina. The intersection of all SNPs on the arrays was used in all subsequent pre-imputation analyses. Before imputation, we excluded SNPs with a Hardy-Weinberg equilibrium *P*-value < 1.0×10^{-6}, call rate of < 95% or MAF of < 1%. The genotypes were then pre-phased using Shapeit2 and imputed using the 1000 Genomes Phase 1 integrated variant set with Impute2. After imputation, SNPs were excluded if the INFO score was < 0.4. Boys and girls were analyzed separately using a logistic regression of case and control status, adjusting for three eigenvectors, and summary statistics were combined using a fixed effects inverse-variance meta-analysis with METAL[108].

SCOOP is a sub-cohort of the Genetics Of Obesity Study (GOOS) cohort. It includes >1,500 UK European ancestry individuals with severe, early onset obesity (BMI Standard Deviation Score > 3 and obesity onset before the age of 10 years), in whom known monogenic causes of obesity have been excluded (cases with *MC4R* mutations were excluded). Two case-control analyses with SCOOP cases were performed: 1) SCOOP vs. UKHLS for which array (Illumina HumanCoreExome) data was available, and 2) SCOOP vs. INTERVAL, for whom whole-exome sequencing data was available.

For the array based analyses, UKHLS controls were genotyped on the Illumina HumanCoreExome-12v1-0 Beadchip. SCOOP cases and 48 UKHLS controls were genotyped on the Illumina HumanCoreExome-12v1-1 Beadchip. The 48 overlapping UKHLS samples were used for quality control to ensure there were no systematic differences and bias between the two versions of the chip. SCOOP and UKHLS samples were phased with SHAPEITv2, and imputed with IMPUTE2 using the combined UK10K-1000G Phase III reference panel. For the WES analyses, SCOOP vs. INTERVAL controls were WES within the UK10K-EXOME project (Agilent v3) and the INTERVAL project (Agilent v5) respectively and

were then jointly called and QC-ed on the union of the sequencing baits. Individuals overlapping or related between the array based and WES studies were removed.

After QC, 1,456 SCOOP and 6,460 UKHLS (BMI range 19-30), and 521 SCOOP and 4,057 INTERVAL individuals were available for the two analyses, all were unrelated, of high quality, and of European ancestry. For both analyses (i.e. SCOOP vs. UKHLS and SCOOP vs. INTERVAL), a maximum likelihood frequentist association test with the additive genetic model was implemented in SNPTEST v2.5. In the SCOOP vs. UKHLS analysis, sex and the first six PCs were included as covariates and variants with a SNPTEST INFO score <0.4 and HWE $p<10^{-6}$ were removed. For the SCOOP vs INTERVAL analysis, we performed an unadjusted analysis (adjustment for PCs did not change sufficiently the results) and variants were limited to those covered at ≥7x in at least 80% of each sequencing cohort, meeting the VQSR threshold of –2.52, missingness <80%, HWE *P*-value$<10^{-8}$, and GQ ≥30.

Cross-trait analyses. We evaluated each of the 14 R/LF SNVs for their association with other relevant obesity-related traits and conditions. We performed lookups in ExomeChip meta-analysis results from other consortia, including, our own GIANT consortium (height[15], WHR adjusted for BMI[24]), MAGIC (HbA1c, Fasting Insulin, Fasting Glucose, 2-hour glucose), GLGC (HDL-cholesterol (HDL-C), LDL-cholesterol (LDL-C), triglycerides and total cholesterol)), IBPC[40] (systolic and diastolic blood pressure), REPROGEN[23] (age at menarche and menopause) and GoT2D/T2D-GENES[16] (type 2 Diabetes). Associations were considered significant at $P < 2.0\times10^{-5}$, accounting for multiple testing.

Phenome-wide association analysis (PheWAS). To evaluate the potential for pleiotropic effects for SNPs discovered from primary analyses, we performed phenome-wide association studies (PheWASs) using genotype and phenotype data from two independent sources of electronic health records (EHR): Vanderbilt University Medical Center Biorepository (BioVU) and the United Kingdom BioBank (UKBB). Phenotype selection and analysis strategy were synchronized across sites. A total of 1502 hierarchical phenotype codes from EHRs were curated by grouping International Classification of Disease, Ninth Revision (ICD-9) clinical/billing codes as previously described[110]. Phenotype codes with 20 or more cases and with minor

allele count of 5 or greater in cases and controls were eligible for analysis. Series of logistic regression analyses were then performed in individuals of European ancestry for each eligible phenotype-genotype combination while adjusting for 5 genetic ancestry PCs. Odds ratios from genotype-phenotype combinations present in both BioVU and UKBB were then aggregated using inverse-variance weighted fixed-effects meta-analysis. Associations with p-values corresponding to false discovery rate (FDR) cut off of less than 10% were considered statistically significant.

Gene set enrichment analysis. We adapted DEPICT, a gene set enrichment analysis method for GWAS data, for use with the ExomeChip ('EC-DEPICT'). DEPICT's primary innovation is the use of "reconstituted" gene sets, where many different types of gene sets (e.g. canonical pathways, protein-protein interaction networks, and mouse phenotypes) were extended through the use of large-scale microarray data (see[111] for details). EC-DEPICT computes *P*-values based on Swedish ExomeChip data (Malmö Diet and Cancer [MDC], All New Diabetics in Scania [ANDIS], and Scania Diabetes Registry [SDR] cohorts, N=11,899) and, unlike DEPICT, takes as input only coding variants and only the genes directly containing those variants, rather than all genes within a specified amount of linkage disequilibrium (**Supplementary Note**).

Four analyses were performed for the BMI EC variants: [1] all coding variants with $P<5x10^{-4}$, [2] all coding variants with $P<5x10^{-4}$ independent of known GWAS variants[5], [3] all coding R/LF variants with $P<5x10^{-4}$, and [4] all coding R/LF variants with $P<5x10^{-4}$ independent of known GWAS variants. Affinity propagation clustering[3] was used to group highly correlated gene sets into "meta-gene sets". For each meta-gene set, the member gene set with the best *P*-value was used as representative for purposes of visualization (**Supplementary Note**). DEPICT for ExomeChip was written using the Python programming language (See URLs).

Drosophila RNAi knockdown experiments. For each of the 13 genes in which R/LF coding variants were associated with BMI, we searched for its corresponding orthologues in *Drosophila* in the ENSEMBL orthologue database. Orthologues were available for nine genes, but missing for *ZBTB7B*, *MC4R*, *GIPR*,

and *ZNF169*. For each of the nine genes, we generated adipose-tissue (cg-Gal4) and neuronal (elav-Gal4) specific RNAi-knockdown crosses, leveraging upstream activation sequence (UAS)-inducible short-hairpin knockdown lines, available through the Vienna Drosophila Resource Center (VDRC). We crossed male UAS-RNAi flies and elav-GAL4 or CG-GAL4 virgin female flies. All fly experiments were carried out at 25 °C. Five-to-seven-day-old males were sorted into groups of 20, weighed and homogenated in PBS with 0,05% Tween with Lysing Matrix D in a beadshaker. The homogenate was heat-inactivated for 10 min in a thermocycler at 70 °C. 10µl of the homogenate was subsequently used in triglyceride assay (Sigma, Serum Triglyceride Determination Kit) which was carried out in duplicates according to protocol, with one alteration: the samples were cleared of residual particulate debris by centrifugation before absorbance reading. Resulting triglyceride values were normalized to fly weight and larval/population density. We used the non-parametric Kruskall-Wallis test to compare wild type with knockdown lines.

Enrichment analysis in monogenic genes of obesity. We identified 39 genes with strong evidence that disruption causes monogenic or syndromic forms of obesity (**Supplementary Table 21**). To test whether these genes are enriched for R/LF coding variant associations with BMI, we conducted simulations by matching each of the 39 genes with other genes based on gene length and number of variants tested, to create a matched set of genes. We generated 1,000 matched gene sets from our data and assessed how often the number of R/LF coding variants that exceeded given significance thresholds was greater in our monogenic/syndromic obesity gene set compared to the matched gene sets.

DATA AVAILABILITY

Summary statistics can be downloaded from http://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium

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Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure underpinning obesity

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SUPPLEMENTARY NOTE

1. COMMON CODING VARIANTS ASSOCIATED WITH BMI

The main focus of our study was the analysis of the 215,917 rare and low frequency (R/LF) coding variants, which are more likely to disrupt protein function[1,2]. However, besides R/LF coding variants, the ExomeChip also carries 13,786 common coding SNVs, which were also tested for association with BMI as part of the study.

We identified 41 novel loci that showed association with BMI (AWS: $P<2.0x10^{-7}$), independent from any previously identified loci (**Supplementary Table 4, Supplementary Figure 4**). The reasons why these 41 novel loci has not been reported by previous large-scale GWAS before are; the sample size of the current study is more than twice as large as the most recent GWAS[3], thus providing greater statistical power for discovery, and/or SNPs may not have been tested in previous GWAS efforts because they were not available in HapMap, and thus not imputed, SNPs did not pass quality control, or are located on the X-chromosome, which has so far not been considered in GWAS.

We also identified common variants that clustered in 51 loci that had been identified before (<1Mb previous GWAS lead SNP) in large-scale GWAS efforts of adiposity traits (**Supplementary Table 4, Supplementary Figure 4**). Using conditional analyses (**Online Methods**), we were able to show that 38 of these 51 loci represent the same locus as the one identified before and one represents an independent secondary signal in the previously established locus. For the remaining 12 loci, we were not able to confirm whether the association represented secondary or the same signal within the established locus because the original SNP (or proxy) was not available on the ExomeChip to perform conditional analyses (**Supplementary Table 4, Supplementary Figure 4**).

Effect sizes of the 41 novel loci are smaller (on average 0.014 SD/allele, [range: 0.010 – 0.024 SD/allele]) than those of the 37 previously established loci (average 0.021 SD/allele, [range: 0.010 – 0.050 SD/allele]) (**Supplementary Figure 5**). This difference is likely due to the increased sample size (N>700,000), and thus power, of our meta-analyses, compared to sample size of

previous GWAS efforts (N up to 340,000), allowing the identification of loci with smaller effects. Signals in established loci, for which conditional analyses could not convincingly determine whether it was a secondary observation, have effect sizes in between the novel and established loci (average 0.016 SD/allele, [range: 0.010 – 0.030 SD/allele]). The explained variance of the 41 novel loci ranges between 0.004% and 0.02%, and add up to a combined explained variance of 0.394%, as compared to the 2.7% of the variance explained by the 97 loci reported in our latest GWAS BMI effort[3].

The novel common coding loci have features similar to those of previously established GWAS loci; i.e. they represent a cluster of variants in high LD with each other that require further fine-mapping efforts to identify the causal genes/variants in the locus. The common coding variants, including those that reached $P<5x10^{-4}$, were included in the EC-DEPICT analyses and results are described in the **Main text**.

2. COMPARISON OF NOVEL COMMON, LOW FREQUENCY AND RARE VARIANTS ACROSS ANCESTRIES

2.1. Low-frequency and rare coding SNVs

We observed no significant heterogeneity in effect sizes across ancestries, accounting for multiple testing across novel SNVs ($P_{threshold}$ = $9x10^{-4}$ = 0.05/(14+41)), which may in part be due to low statistical power in non-European ancestry populations **(Supplementary Table 7, Supplementary Figure 6).** Minor allele frequencies are general consistent across ancestries, with two exceptions. The minor allele of rs7636 (p.Pro477Pro) in *ACHE* is of low frequency in European ancestry populations (4.2%), but much more common in African (24.4%) and Hispanic (9.9%) ancestry populations and, similarly, that of rs12236219 in *ZNF169* is of low frequency in European ancestry populations, but common in all other ancestries studied.

Of interest are the two SNVs (p.His353Asn, p.Pro477Pro) in *ACHE,* which track together nearly perfectly in European ancestry populations (r^2=0.98; *D'*=0.99, MAFs=4.2%), whereas in African ancestry populations they are not correlated (r^2=0.01; *D'*=0.95). In the African ancestry

data, the non-synonymous SNV p.His353Asn is rare (0.60%) and has a similar estimated effect size (0.057 SD/allele, 95% CI [-0.050-0.164], *P*=0.29) to the effect seen in European ancestry individuals (0.034 SD/allele, 95% CI [0.023-0.044]), whereas the synonymous p.Pro477Pro is common (24.4%) and has no detectable effect on BMI (-0.006 SD/allele, *P*=0.56). Even though our sample size was relatively small, an effect of 0.023-0.044 SD/allele, as observed in European ancestry individuals, would have been detectable in our African-ancestry population (MAF=24.4%, N~24,000, power ~80%, at α=0.01). The absence of such association suggests that p.Pro477Pro may not be driving the association at this locus and that p.His353Asn (or potentially a variant correlated with p.His353Asn, but not with p.Pro477Pro, in African-ancestry populations) is more likely to be the causal variant. This is consistent with functional role of many non-synonymous, as compared to synonymous variants.

2.2. Novel common SNVs

None of the 41 novel commons SNVs showed evidence of heterogeneity across ancestries ($P_{threshold}$ = $9x10^{-4}$). Generally, allele frequencies of the BMI-increasing allele in European ancestry populations were consistent with those of South Asian (r^2 = 0.82) and Hispanic (r^2 = 0.86) ancestry populations, and somewhat lower with African (r^2 = 0.52) and East Asian (r^2 = 0.48) ancestries **(Supplementary Table 7, Supplementary Figure 6)**. Because of the relatively small sample sizes of non-European ancestry populations, statistical power for replication of associations observed in the total sample or European ancestry only meta-analyses was low. Nevertheless, of the 41 SNVs, associations were directionally consistent for 32 SNVs (78%), of which 7 reached nominal significance, in the African ancestry meta-analysis **(Supplementary Table 7, Supplementary Figure 6)**. The directional consistency between European ancestry associations was similar for South Asian (34 SNVs (83%) of which 5 nominally significant) and Hispanic (34 SNVs (83%) of which 3 nominally significant) ancestry populations, and lower for East Asian ancestry populations (61 SNVs (61%) of which 6 nominally significant).

3. GENE SET ENRICHMENT ANALYSIS (EC-DEPICT)

DEPICT is a method for gene set enrichment analysis and gene prioritization of GWAS data[4]. Briefly, 14,462 gene sets from KEGG[5], REACTOME[6], Gene Ontology[7], InWeb[8] (protein-protein networks) and Mouse Phenotype[9] databases were obtained and "reconstituted" using large-scale microarray data, based on the logic of guilt-by-association (genes with similar patterns of expression are more likely to be members of the same gene sets). We have adapted the gene set enrichment functionality of DEPICT for the ExomeChip (EC-DEPICT), with a few alterations: (1) instead of including all genes within a specified amount of linkage disequilibrium to each index SNP, we include only the gene containing the index SNV, (2) we include only nonsynonymous and splicing (coding) SNVs, discarding noncoding associations and (3) we use null ExomeChip data for p-value calculation (rather than null GWAS data). In this supplement, we provide a brief overview of the method and more detailed explanations of each analysis.

3.1. Method

The EC-DEPICT method has been described elsewhere[10]. We generated null ExomeChip data from the Malmö Diet and Cancer (MDC), All New Diabetics in Scania (ANDIS), and Scania Diabetes Registry (SDR) cohorts (a total of 11,899 samples with Swedish ancestry). After generating simulated normally-distributed phenotypes, we conducted 2,200 null ExomeChip association studies, filtering out all variants not present in the BMI association study. The variants in each null study were then sorted by ascending *P*-value and clumped (+/- 1 Mb on each side). Annotations from the CHARGE consortium were used to assign variants to genes (see URLs). For analyses of rare/low-frequency variants, a separate set of backgrounds was created that retained only loci where the index SNV had a minor allele frequency of <5%.

The method for gene set enrichment is as follows. A list of significant input variants from the ExomeChip is obtained (index SNVs for each locus, coding variants only) and filtered to remove variants not present in the null backgrounds or that are not marked as nonsynonymous/splice-site in the CHARGE consortium annotations. Then, we map the variants

to genes. For each gene set, we then calculate a test statistic: the sum of gene set membership z-scores from the reconstituted gene sets[1] for the input genes. We then take 2000 nulls and compute the average (null) test statistic and standard deviation for the given gene set (where the number of top genes we take from each null as "input genes" is matched to the observed number of input genes). A z-score for the gene set is then computed as the observed test statistic minus the null test statistic divided by the null standard deviation, which is converted to a p-value based on the normal distribution. False discovery rates (FDRs) were calculated using an additional 50 null permutations to generate a distribution of null p-values. The FDR was calculated as the average number of null p-values less than a given threshold divided by the number of observed p-values less than that threshold.

Our null data (MDC, ANDIS, and SDR cohorts) was also used for the ExomeChip analysis of height[10]. As in the height analysis, before gene set enrichment analysis of BMI-associated variants, we removed variants absent in this null ExomeChip data. This resulted in exclusion of about 30% of the BMI-associated variants at suggestive of array-wide significance. Most of the excluded variants were in the very rarest allele frequency bins, and mostly reached suggestive rather than array-wide significance. The exclusion of the rarest variants is expected due to the much smaller sample size of the null cohorts relative to the BMI data. To try to include more variants in the analysis, we also generated null ExomeChip data based on the UK Biobank, which resulted in the exclusion of fewer BMI-associated variants (due to the much larger sample size of the UK Biobank data). However, we observed that use of these null data, despite including more of the rarest BMI-associated variants in the gene set enrichment analysis, dampened the signal and resulted in fewer significantly enriched gene sets. This result suggests that 1) the rarest variants are more likely to have a lower true positive rate and/or 2) the heterogeneity of the underlying biology increases with the inclusion of very rare variants.

Although some variants were excluded from the EC-DEPICT analysis, we have included them in the heatmap figures (Figure 2, Supplementary Figure 10). This is because we assume

that if the genes containing those variants have strong predicted membership in gene sets found to be significantly enriched, they are still good candidates for prioritization (and one of the main purposes of the heatmap strategy is to visually prioritize the best candidate genes). In fact, this is arguably even stronger evidence for prioritization of these genes, because they had no opportunity to influence the gene sets that are identified as enriched and, as such, independently support the biology implicated by these gene sets.

We have observed that extreme non-normality of gene set membership z-scores can, in certain situations, cause minor inflation of Type I error. To address this issue, we repeated the original EC-DEPICT analysis with an inverse-normal-transformed version of the reconstituted gene sets, in which every gene set is forced to have a normal z-score distribution for pathway membership. We then compared the rank of each significant gene set in the original results with the rank in the inverse normal transform and flagged "outliers" with respect to the change in rank (> 1.5 * the interquartile range). In visualizing the results with heat maps and in supplementary tables, outlier gene sets were excluded.

3.2. Analyses

We performed four different analyses of the BMI-associated variants. In each case, for each locus, we included the best coding variant, including secondary signals if present. "GWAS-independent" analyses were performed by excluding EC loci conditionally dependent on or <1 Mb away from a known GWAS locus (see below for details). For this purpose, "known loci" consisted of a list of all variants used as input in the original DEPICT analysis in Locke et al.[3] ($P<5x10^{-4}$). This was necessary to confirm true independence from the original DEPICT findings (i.e. gene set enrichment results for EC that come from a completely non-overlapping set of genes relative to the original DEPICT analysis).

The breakdown of included variants is as follows. Array-wide significant variants ($P<2x10^{-7}$) came from the final meta-analysis of Discovery, deCODE, and UK Biobank results across all analysis strata. For these variants ("stringent"), independence from genome-wide significant

GWAS loci was determined by conditional analysis. Additional variants with p-values between $5x10^{-4}$ and $2x10^{-7}$ ("relaxed") were based on Discovery in the all-ancestries sex-combined additive model. For these variants, independence from genome-wide significant GWAS loci was based on a distance of >1 Mb. For both stringent and relaxed variants, independence from marginally significant GWAS loci was also based on a distance of > 1 Mb. All loci were clumped +/- 1 Mb.

For the first analysis, we included all EC loci with $p<5x10^{-4}$. After filtering, this left 244 variants in 242 genes; we discovered 67 gene sets (24 meta-gene sets) at FDR <0.05. After removing inverse normal transform outliers (see description above), that left 62 gene sets (still in 24 meta-gene sets). The second analysis included EC loci with $5x10^{-4}$ "independent" of a known GWAS locus[3] (110 variants in 110 genes after filtering). We found no significant gene sets in this analysis.

The third and fourth analyses included rare and low-frequency (RLF; <5% MAF) variants only. The third analyses included all RLF variants with $P<5x10^{-4}$, representing a total of 50 variants in 50 genes after filtering. We found 512 significant gene sets at FDR <0.05 (107 meta-gene sets). After applying the inverse normal transform filter, this was reduced to 471 significant gene sets in 106 meta-gene sets. Finally, the last analysis included RLF variants with $P<5x10^{-4}$ "independent" of a known GWAS locus[3] (after filtering, 30 variants in 30 genes). This recovered 31 significant gene sets in 12 meta-gene sets at FDR <0.05. After the inverse normal transform, we retained 29 significant gene sets, still in 12 meta-gene sets.

3.3. Affinity propagation clustering

To collapse the most highly correlated gene sets, affinity propagation clustering was performed as described in Marouli et al. (2017)[10]. Briefly, "meta-gene sets" were generated by affinity propagation clustering[3] of all pairs of 14,462 gene sets, using SciKit-Learn.clustering.AffinityPropagation version 0.17[11], with a maximum iteration of 10,000 and a convergence iteration of 1,000. For each meta-gene set, *P*-values were assigned based on the most significant member gene set (considered the "best representative gene set"). In heat maps,

z-scores for meta-gene set membership represent the z-score of the best representative gene set. Heat maps were generated with the ComplexHeatmap package in R[12]. For Online Mendelian Inheritance in Man (OMIM) annotations, a manual curation of obesity-related terms in the OMIM database was performed.

3.4. URLs

CHARGE Consortium ExomeChip annotation file:

http://www.chargeconsortium.com/main/exomechip/

EC-DEPICT: https://github.com/RebeccaFine/obesity-ec-depict

EC-DEPICT meta-gene sets: https://github.com/RebeccaFine/obesity-ec-depict/blob/master/data/metacluster_labels.txt

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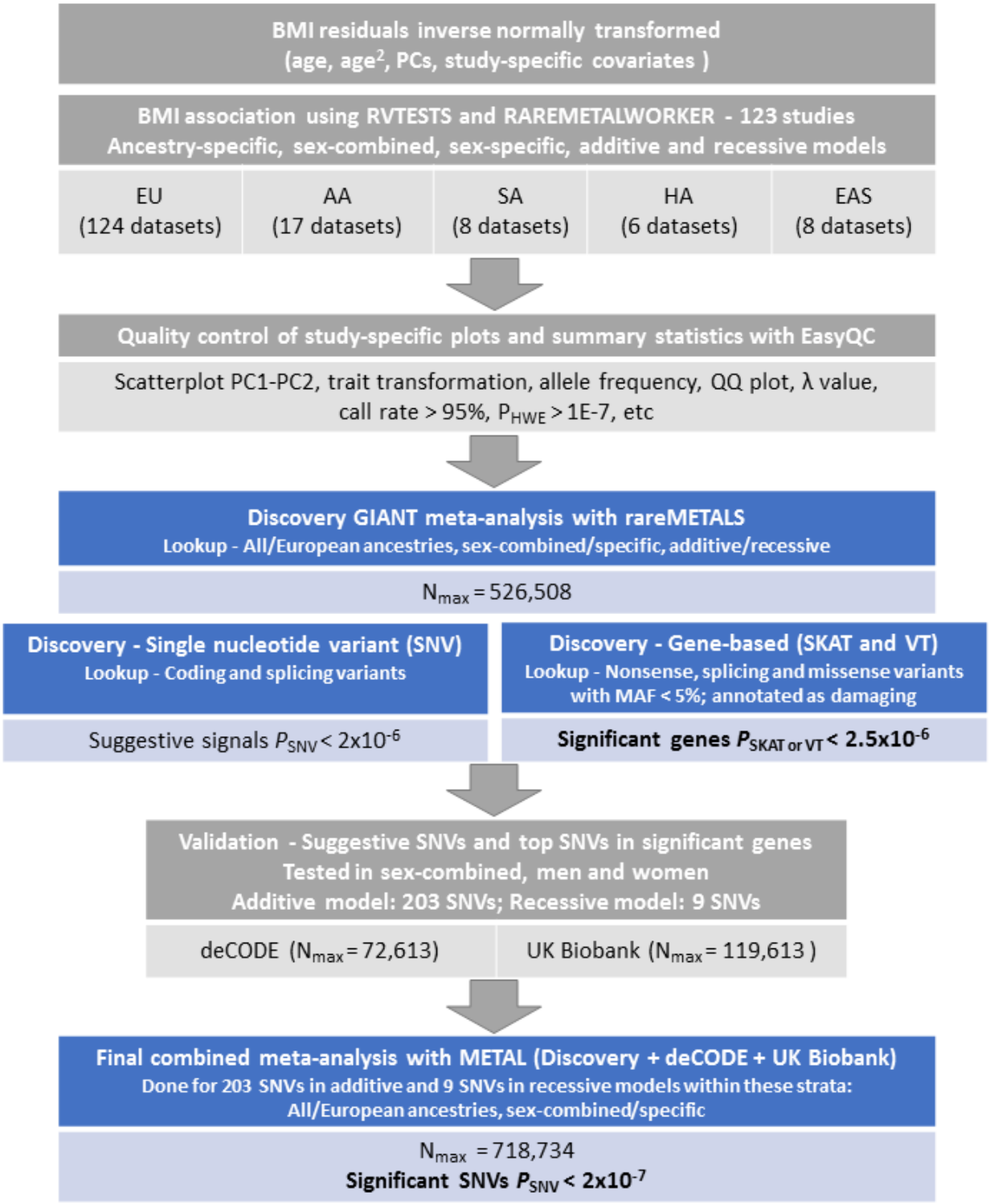
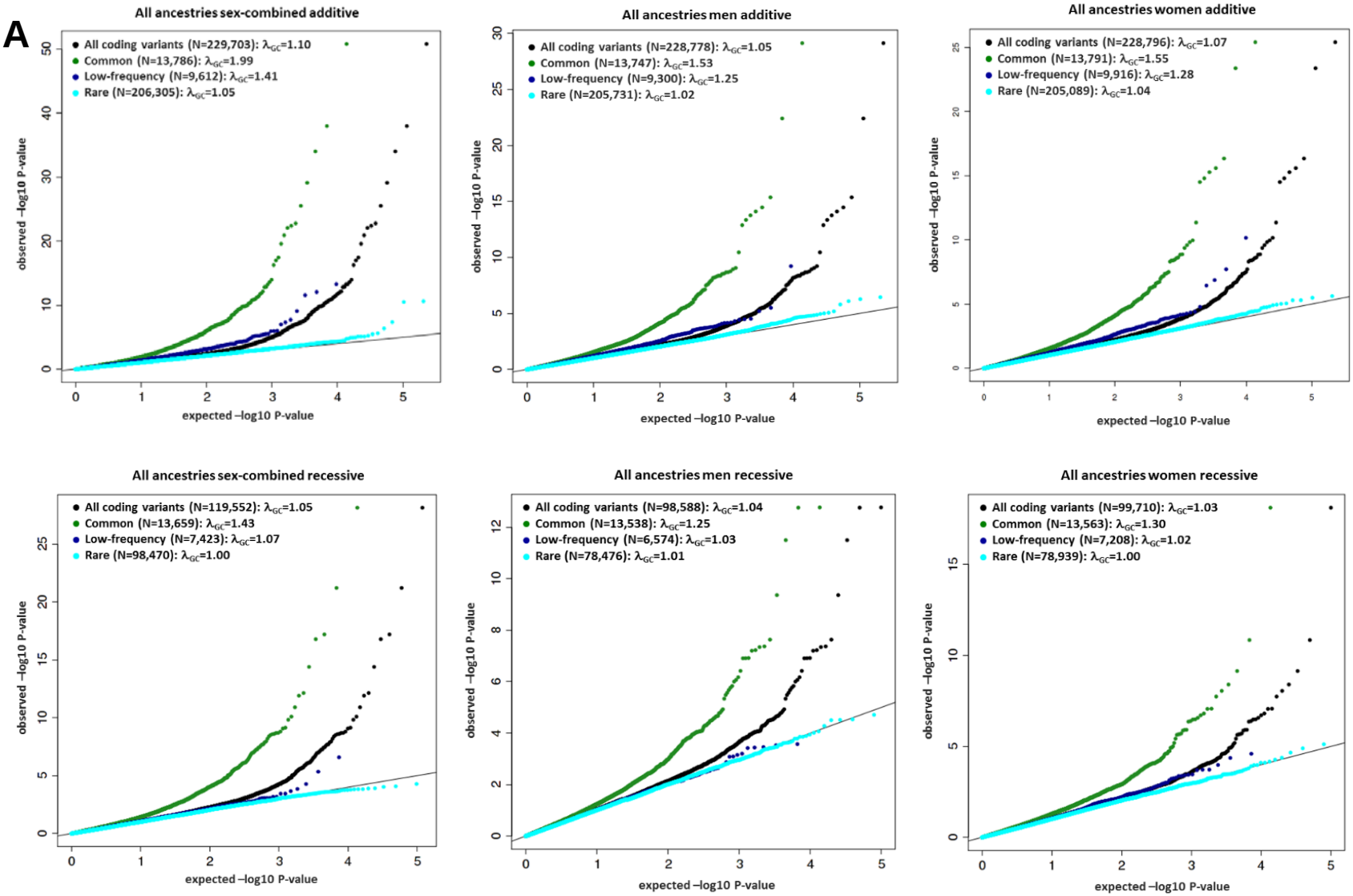
4. SUPPLEMENTARY FIGURES

Supplementary Figure 1 | Flowchart of the GIANT ExomeChip BMI study design.



Supplementary Figure 2 | Quantile-quantile plots of BMI associations for coding SNVs tested in the Discovery GIANT meta-analyses. A-B. Quantile-quantile plots of BMI associations tested in all-ancestries (**A**) and European ancestry (**B**) strata for all coding (exonic and splicing) SNVs in black, and stratified by minor allele frequency (MAF) cut-offs; common variants (MAF≥5%) in green, rare and low-frequency variants (MAF<5%) in dark blue, and rare variants (MAF<1%) in light blue. **C-D.** Quantile-quantile plots of BMI associations tested in all-ancestries (C) and European ancestry (D) strata for all coding (exonic and splicing) SNVs in black, and after excluding (±1Mb) known and novel loci identified in previous BMI GWAS and in the ExomeChip meta-analysis (pink).

A


All ancestries sex-combined additive
All coding variants (N=229,703): λGC=1.10
Common (N=13,786): λGC=1.99
Low-frequency (N=9,612): λGC=1.41
Rare (N=206,305): λGC=1.05
All ancestries men additive
All coding variants (N=228,778): λGC=1.05
Common (N=13,747): λGC=1.53
Low-frequency (N=9,300): λGC=1.25
Rare (N=205,731): λGC=1.02
All ancestries women additive
All coding variants (N=228,796): λGC=1.07
Common (N=13,791): λGC=1.55
Low-frequency (N=9,916): λGC=1.28
Rare (N=205,089): λGC=1.04
All ancestries sex-combined recessive
All coding variants (N=119,552): λGC=1.05
Common (N=13,659): λGC=1.43
Low-frequency (N=7,423): λGC=1.07
Rare (N=98,470): λGC=1.00
All ancestries men recessive
All coding variants (N=98,588): λGC=1.04
Common (N=13,538): λGC=1.25
Low-frequency (N=6,574): λGC=1.03
Rare (N=78,476): λGC=1.01
All ancestries women recessive
All coding variants (N=99,710): λGC=1.03
Common (N=13,563): λGC=1.30
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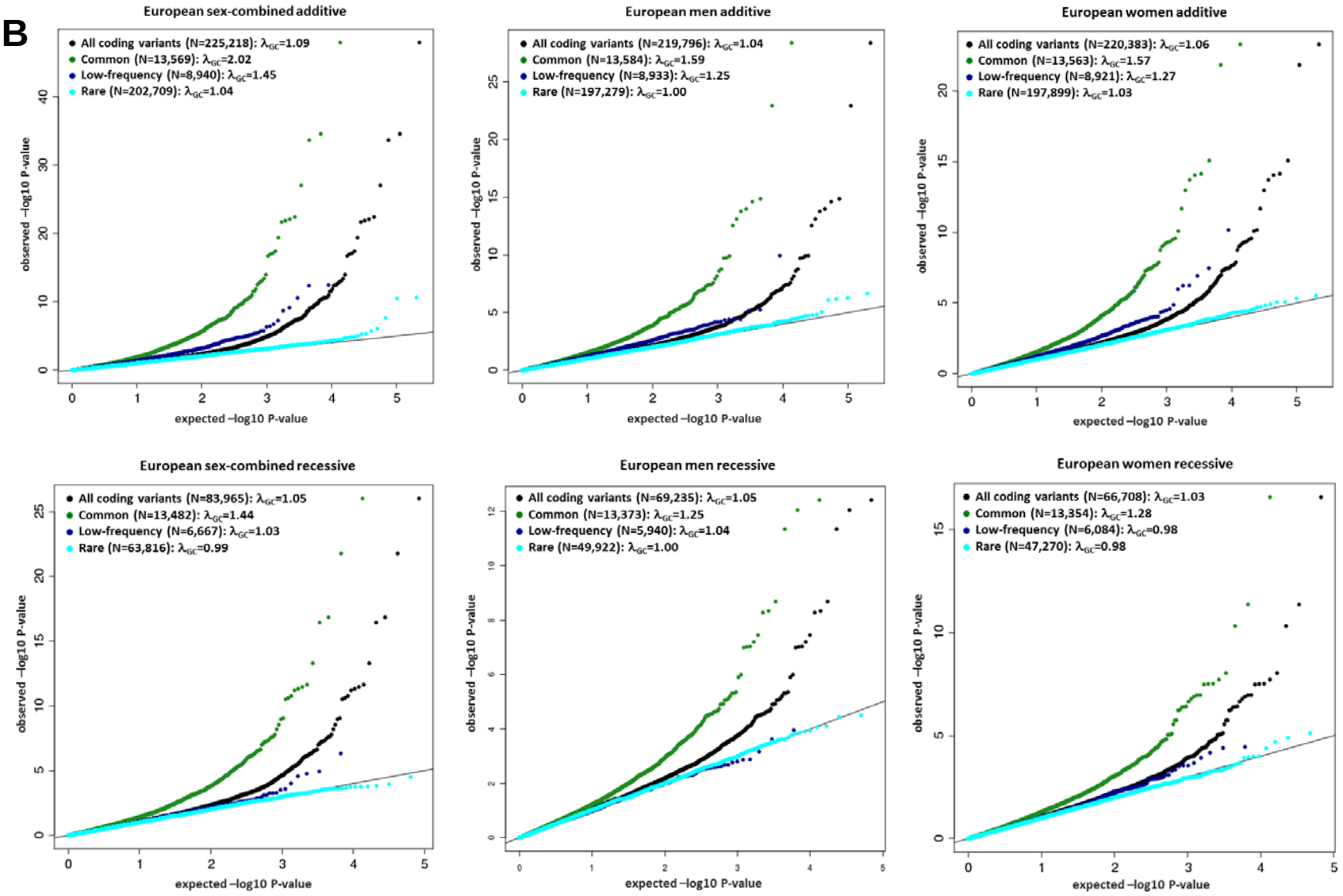
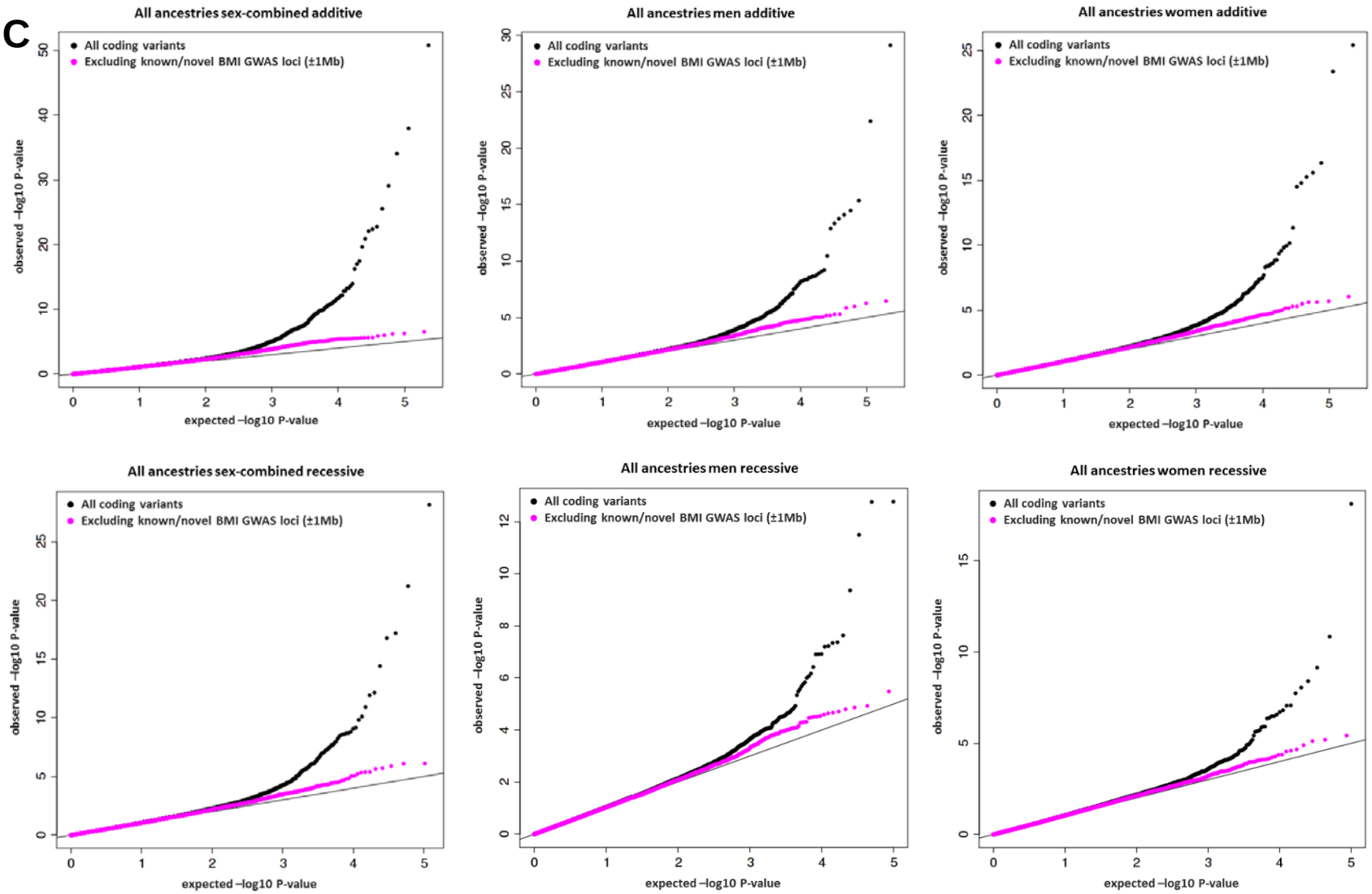
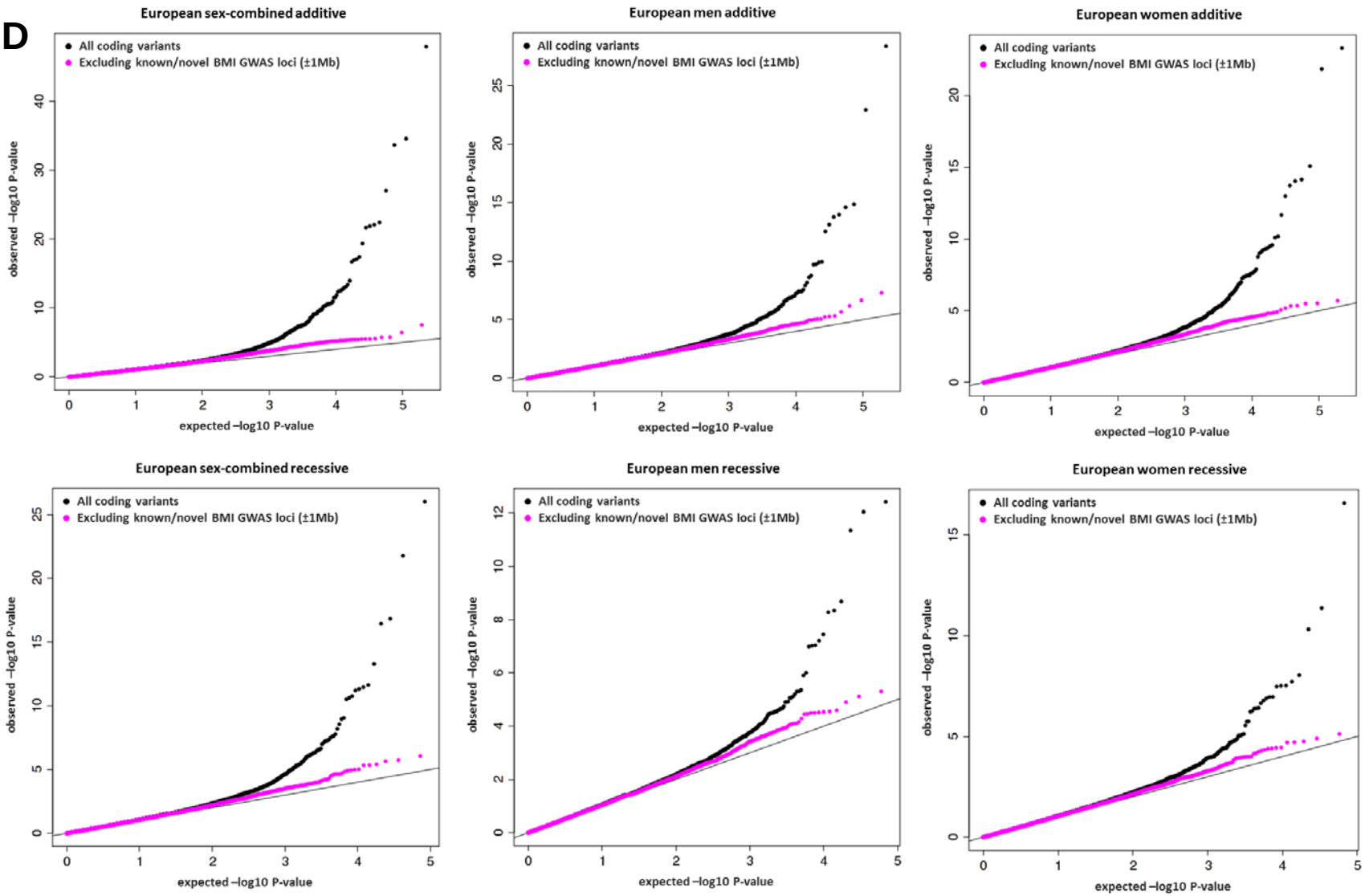
Rare (N=78,939): λGC=1.00
observed –log10 P-value
expected –log10 P-value

B

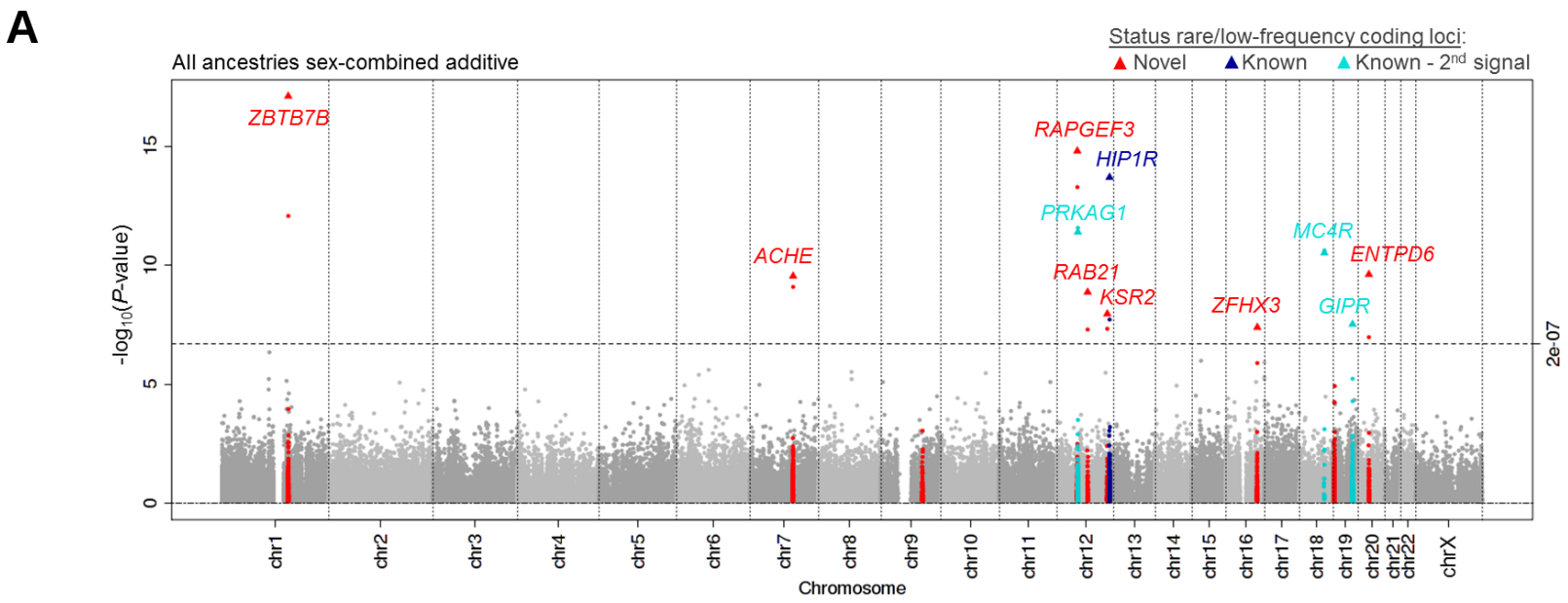

European sex-combined additive
All coding variants (N=225,218): λGC=1.09
Common (N=13,569): λGC=2.02
Low-frequency (N=8,940): λGC=1.45
Rare (N=202,709): λGC=1.04
European men additive
All coding variants (N=219,796): λGC=1.04
Common (N=13,584): λGC=1.59
Low-frequency (N=8,933): λGC=1.25
Rare (N=197,279): λGC=1.00
European women additive
All coding variants (N=220,383): λGC=1.06
Common (N=13,563): λGC=1.57
Low-frequency (N=8,921): λGC=1.27
Rare (N=197,899): λGC=1.03
European sex-combined recessive
All coding variants (N=83,965): λGC=1.05
Common (N=13,482): λGC=1.44
Low-frequency (N=6,667): λGC=1.03
Rare (N=63,816): λGC=0.99
European men recessive
All coding variants (N=69,235): λGC=1.05
Common (N=13,373): λGC=1.25
Low-frequency (N=5,940): λGC=1.04
Rare (N=49,922): λGC=1.00
European women recessive
All coding variants (N=66,708): λGC=1.03
Common (N=13,354): λGC=1.28
Low-frequency (N=6,084): λGC=0.98
Rare (N=47,270): λGC=0.98
observed −log10 P-value
expected −log10 P-value


C
All ancestries sex-combined additive
All ancestries men additive
All ancestries women additive
All ancestries sex-combined recessive
All ancestries men recessive
All ancestries women recessive
All coding variants
Excluding known/novel BMI GWAS loci (±1Mb)
observed −log10 P-value
expected −log10 P-value

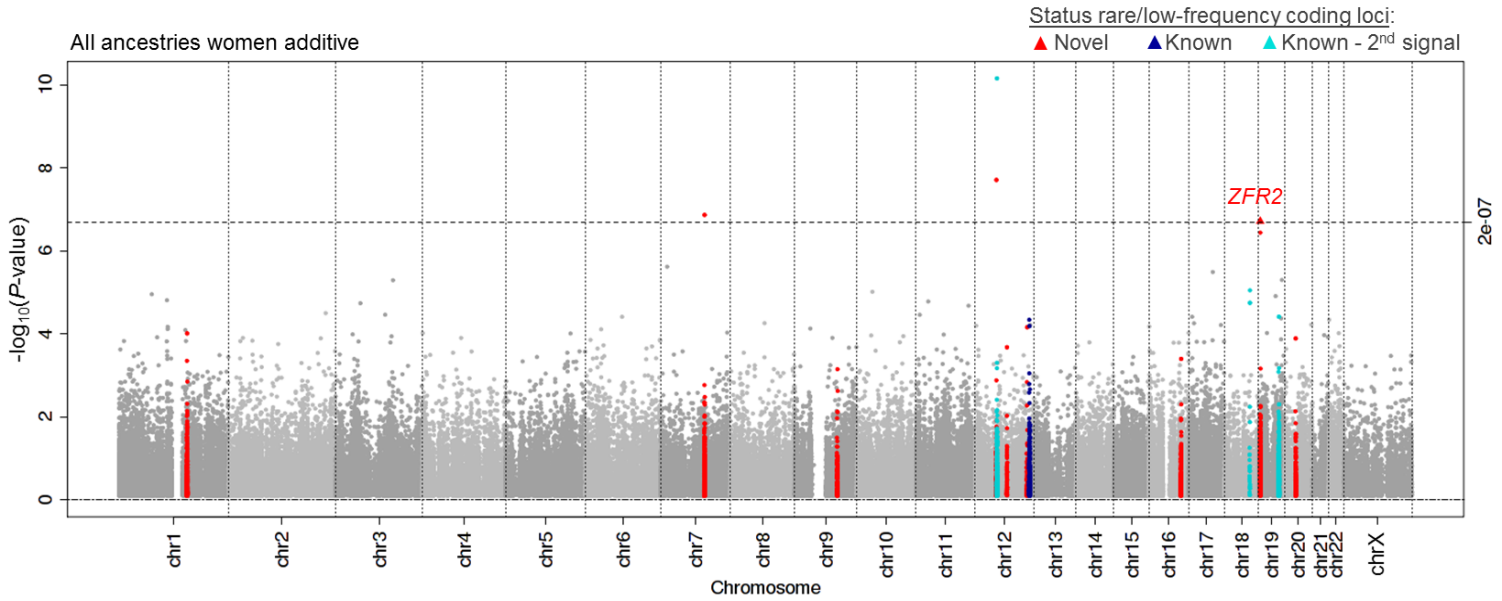
D


European sex-combined additive
European men additive
European women additive
European sex-combined recessive
European men recessive
European women recessive
All coding variants
Excluding known/novel BMI GWAS loci (±1Mb)
observed −log10 P-value
expected −log10 P-value

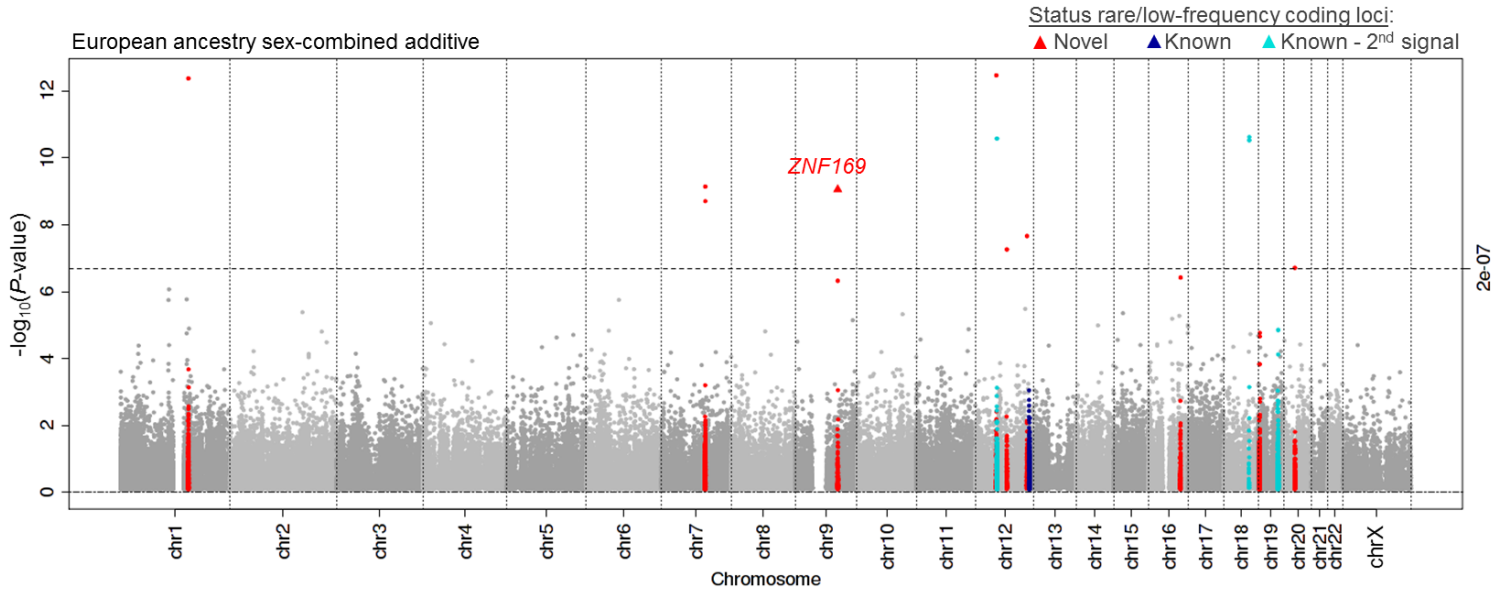
Supplementary Figure 3 | Manhattan plots of coding rare and low-frequency SNV associations in the Discovery GIANT dataset appended with the significant SNVs from the final combined meta-analysis. Manhattan plot of associations in all-ancestries sex-combined additive (A), all-ancestries women additive (B) and European ancestry sex-combined additive (C) strata. Each locus was defined using a 1Mb window on each side of the lead coding variant. Dots correspond to the Discovery GIANT meta-analysis results, while the final combined meta-analysis results were appended to the plots using triangles. Only significant loci in the final combined meta-analysis were colored; novel loci, secondary signals (in known GWAS loci, but independent from GWAS hit/proxy) and known loci were highlighted in red, light blue and dark blue, respectively.



B


All ancestries women additive
Status rare/low-frequency coding loci:
Novel
Known
Known - 2nd signal
ZFR2
2e-07
-log10(P-value)
Chromosome
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX

C

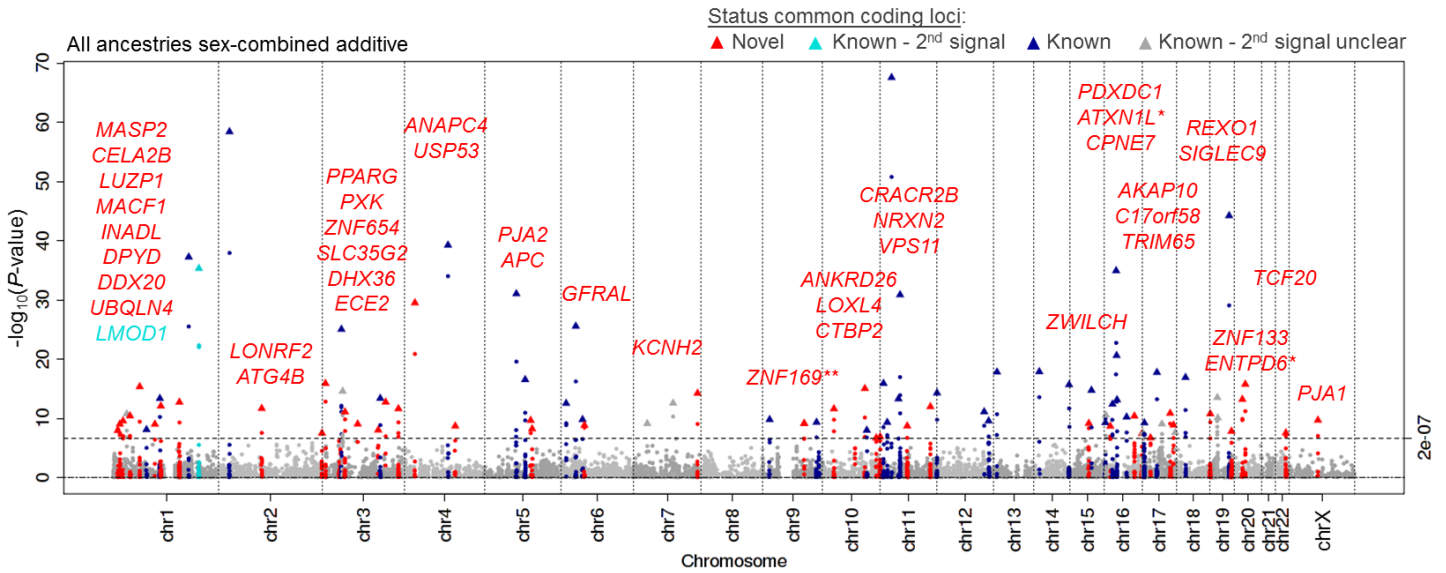

European ancestry sex-combined additive
Status rare/low-frequency coding loci:
Novel
Known
Known - 2nd signal
ZNF169
2e-07
-log10(P-value)
Chromosome
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX

Supplementary Figure 4 | Manhattan plots of coding common SNV associations obtained in the Discovery GIANT dataset appended with the significant SNVs from the final combined meta-analysis See also Supplementary Table 4 for detailed results. Each locus was defined using a 1Mb window on each side of the lead coding variant. Dots correspond to the Discovery GIANT meta-analysis results, while the final combined meta-analysis results were appended to the plots using triangles.

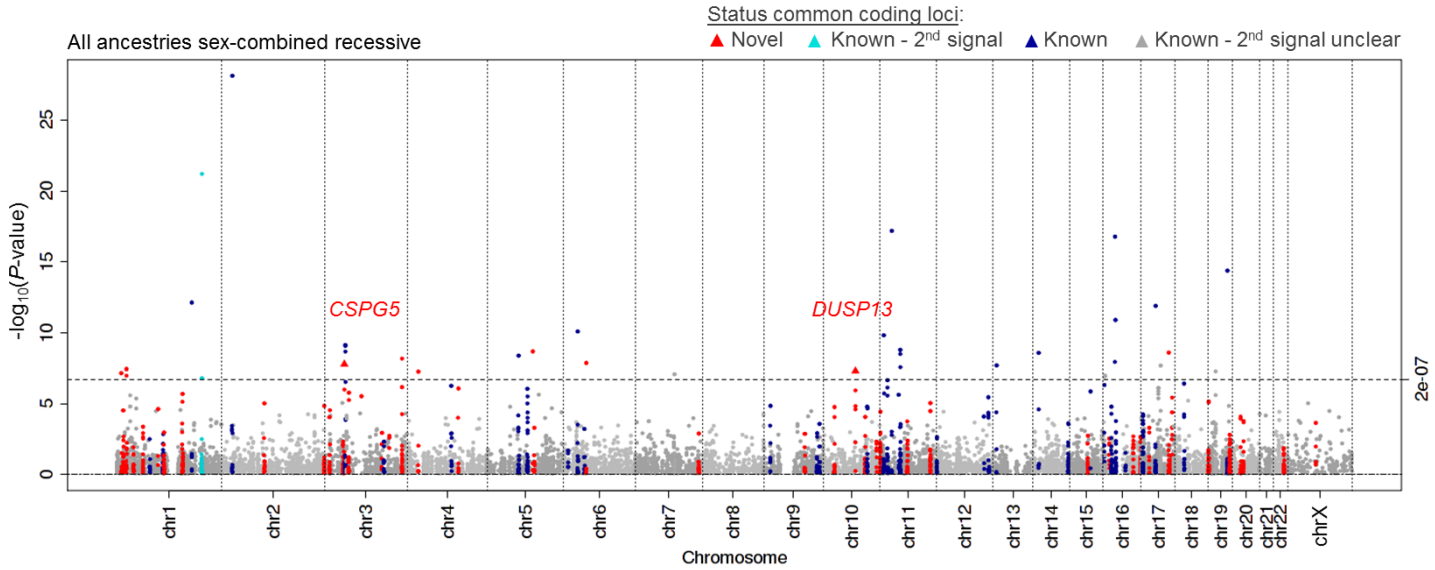
Panels A, B & C: Results from novel loci and novel secondary signals. Manhattan plot of associations in all-ancestries sex-combined additive (A), all-ancestries sex-combined recessive (B) and European ancestry sex-combined additive (C) strata. Only novel loci (in red) and novel secondary signals in known loci (in cyan) are shown in panels A, B & C.

Panels D & E: Results from known loci, some of which with potential secondary signals. Manhattan plot of associations in all-ancestries sex-combined additive (D) and all-ancestries women additive (E) strata. Loci that were previously established (in blue), and signals in previously known loci, but for which conditional analyses could not convincingly determine whether the signal was secondary or the same locus (in grey) are shown in panels D & E.

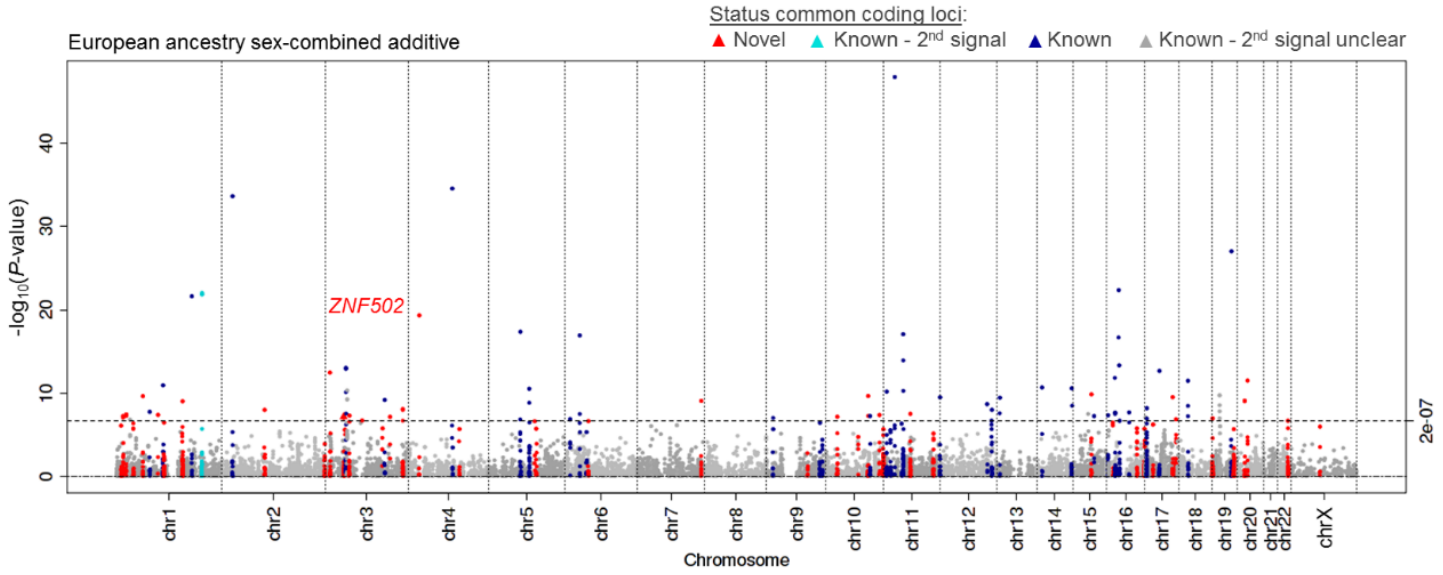
A


All ancestries sex-combined additive
Status common coding loci:
Novel
Known - 2nd signal
Known
Known - 2nd signal unclear
-log10(P-value)
Chromosome
2e-07
MASP2
CELA2B
LUZP1
MACF1
INADL
DPYD
DDX20
UBQLN4
LMOD1
LONRF2
ATG4B
PPARG
PXK
ZNF654
SLC35G2
DHX36
ECE2
ANAPC4
USP53
PJA2
APC
GFRAL
KCNH2
ZNF169**
ANKRD26
LOXL4
CTBP2
CRACR2B
NRXN2
VPS11
PDXDC1
ATXN1L*
CPNE7
REXO1
SIGLEC9
AKAP10
C17orf58
TRIM65
ZWILCH
TCF20
ZNF133
ENTPD6*
PJA1

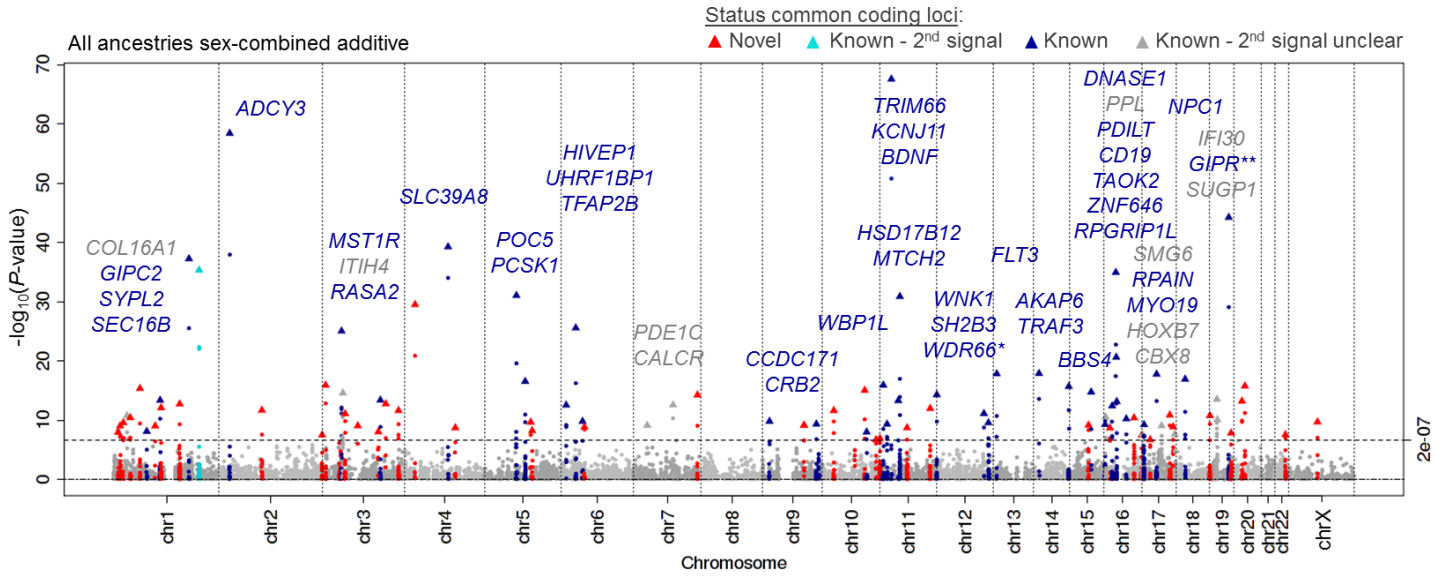
B


All ancestries sex-combined recessive
Status common coding loci:
Novel
Known - 2nd signal
Known
Known - 2nd signal unclear
-log10(P-value)
Chromosome
2e-07
CSPG5
DUSP13

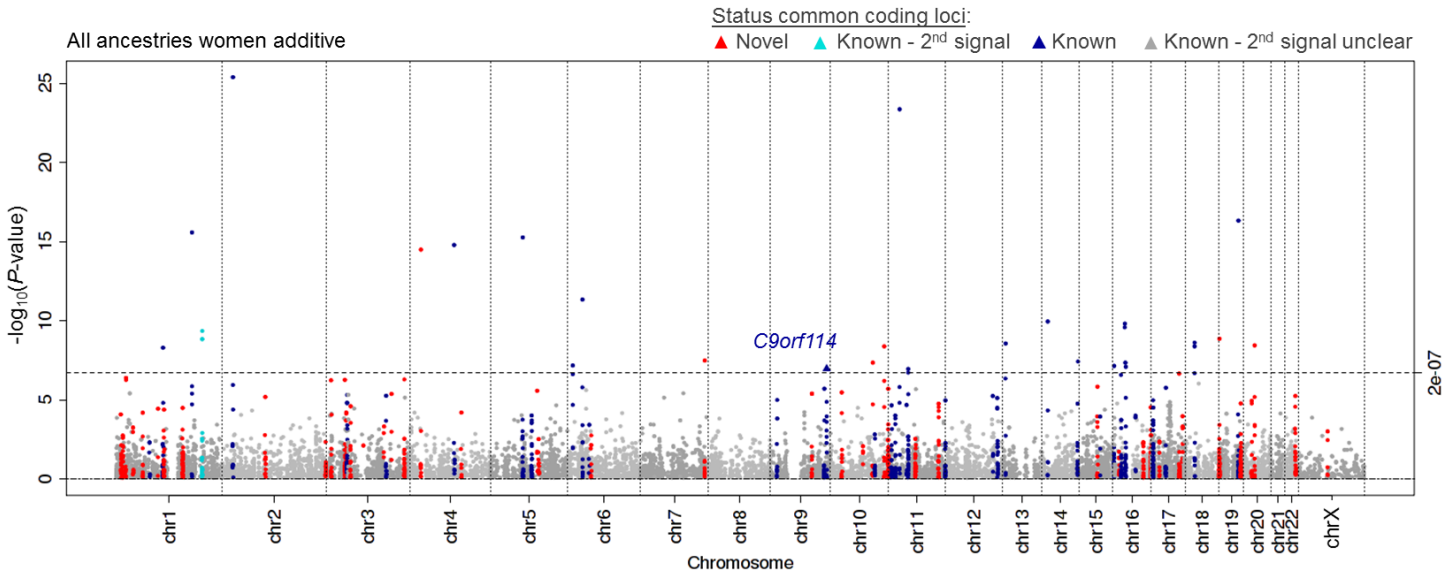
C


Status common coding loci:
Novel
Known - 2nd signal
Known
Known - 2nd signal unclear
European ancestry sex-combined additive
-log10(P-value)
ZNF502
2e-07
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
Chromosome

D

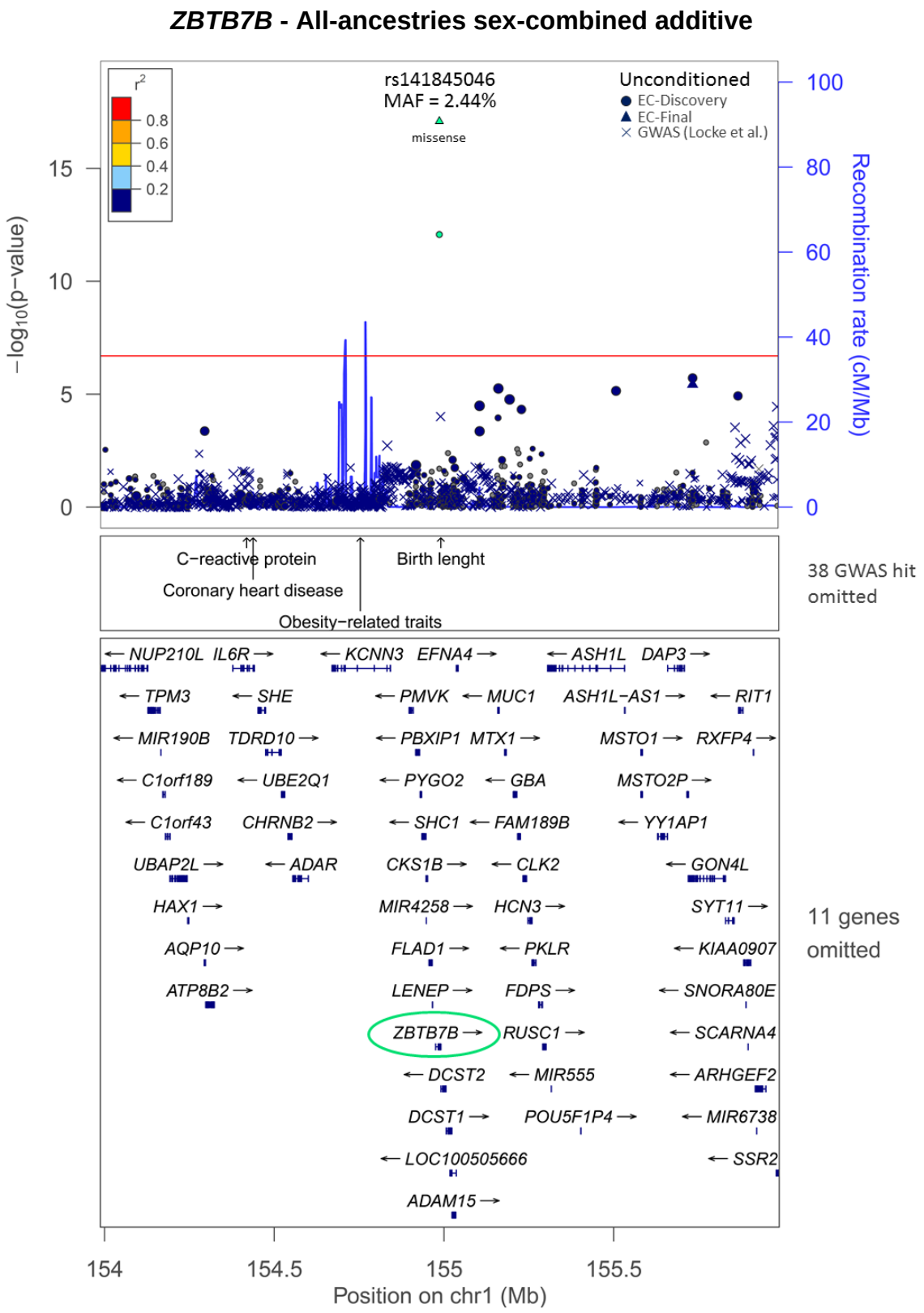

Status common coding loci:
Novel
Known - 2nd signal
Known
Known - 2nd signal unclear
All ancestries sex-combined additive
-log10(P-value)
ADCY3
COL16A1
GIPC2
SYPL2
SEC16B
MST1R
ITIH4
RASA2
SLC39A8
POC5
PCSK1
HIVEP1
UHRF1BP1
TFAP2B
PDE1C
CALCR
CCDC171
CRB2
WBP1L
TRIM66
KCNJ11
BDNF
HSD17B12
MTCH2
WNK1
SH2B3
WDR66*
FLT3
AKAP6
TRAF3
BBS4
DNASE1
PPL
PDILT
CD19
TAOK2
ZNF646
RPGRIP1L
NPC1
IFI30
GIPR**
SUGP1
SMG6
RPAIN
MYO19
HOXB7
CBX8
2e-07
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
Chromosome

E

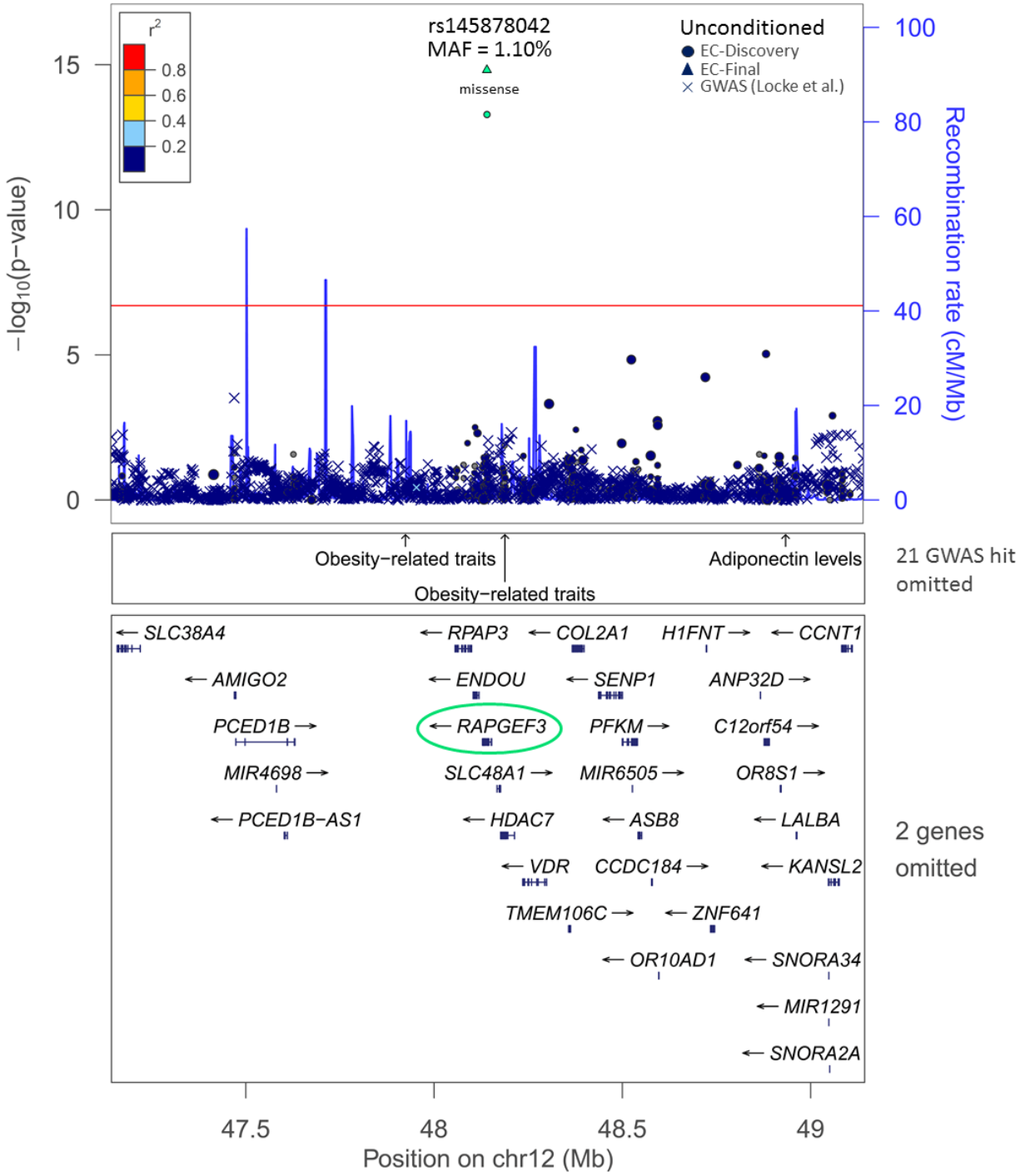

All ancestries women additive
Status common coding loci:
Novel
Known - 2nd signal
Known
Known - 2nd signal unclear
-log10(P-value)
C9orf114
2e-07
Chromosome
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX

Supplementary Figure 5 | Regional association plots for the significant rare and low-frequency coding loci identified in the final combined meta-analysis among all analysis strata. The association results shown in these plots are from the Discovery GIANT meta-analysis in the specified analysis strata for all ExomeChip SNVs (dots) and appended with the previous BMI GWAS results (European ancestry) from Locke et al. (crosses; Locke et al. Nature 518, 197-206). The size of the dots and crosses are weighted on the minor allele frequency. We have used the UK Biobank dataset (European ancestry; N=136,727) to calculate the linkage disequilibrium between the SNVs in the window and the reference coding SNV shown in turquoise. Only GWAS traits related with body weight are shown in the plots. (A) Regional plots for loci with only one significant coding SNV in the region (only unconditioned results shown). (B) Regional plots for loci with more than one significant coding SNVs or with a GWAS hit or proxy (r^2>0.80 in EUR 1000G phase 3) in the region (<±1MB). Both unconditioned and conditioned results are shown.

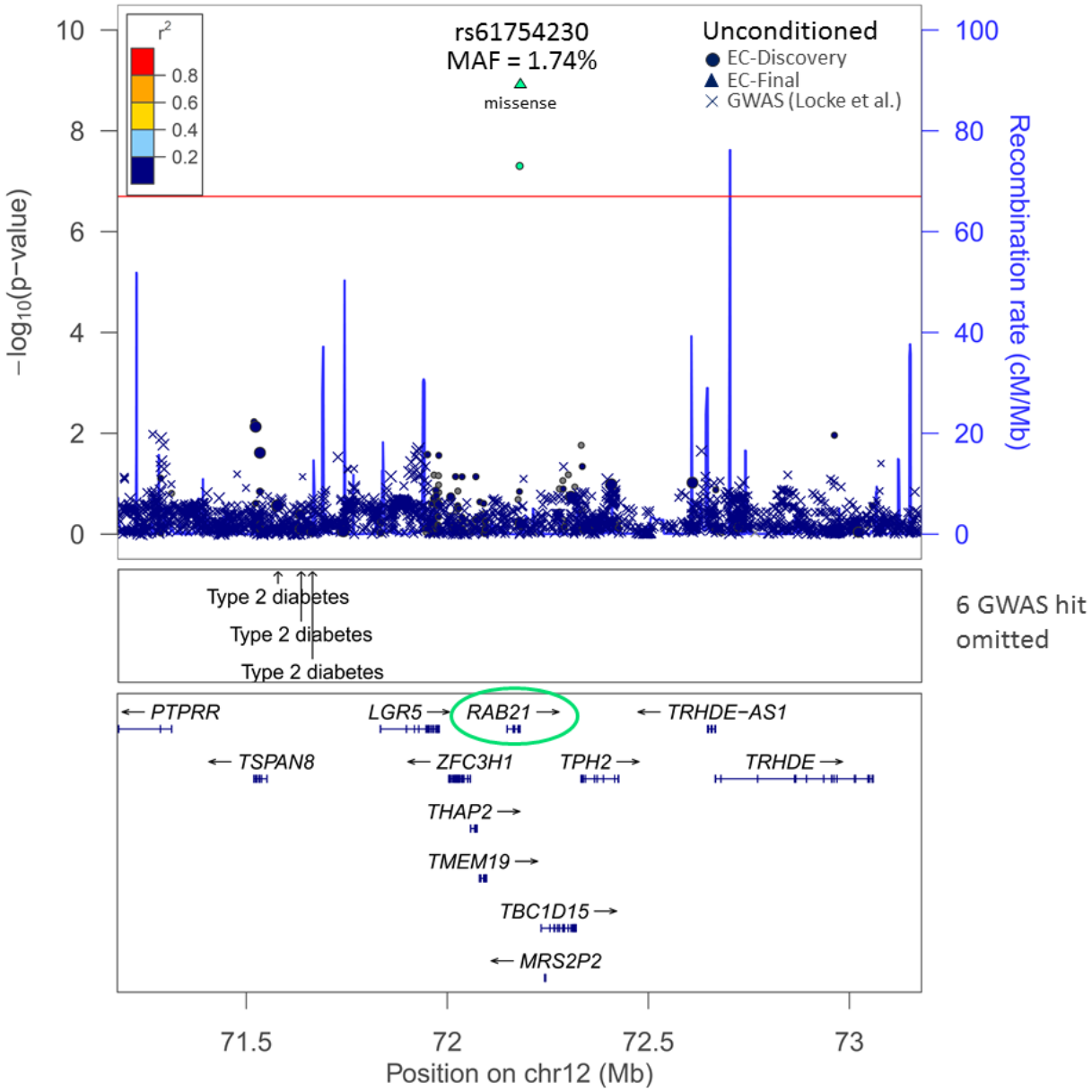
A


ZBTB7B - All-ancestries sex-combined additive
rs141845046
MAF = 2.44%
missense
Unconditioned
EC-Discovery
EC-Final
GWAS (Locke et al.)
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
C−reactive protein
Coronary heart disease
Birth lenght
Obesity−related traits
38 GWAS hit omitted
11 genes omitted
NUP210L
IL6R
KCNN3
EFNA4
ASH1L
DAP3
TPM3
SHE
PMVK
MUC1
ASH1L−AS1
RIT1
MIR190B
TDRD10
PBXIP1
MTX1
MSTO1
RXFP4
C1orf189
UBE2Q1
PYGO2
GBA
MSTO2P
C1orf43
CHRNB2
SHC1
FAM189B
YY1AP1
UBAP2L
ADAR
CKS1B
CLK2
GON4L
HAX1
MIR4258
HCN3
SYT11
AQP10
FLAD1
PKLR
KIAA0907
ATP8B2
LENEP
FDPS
SNORA80E
ZBTB7B
RUSC1
SCARNA4
DCST2
MIR555
ARHGEF2
DCST1
POU5F1P4
MIR6738
LOC100505666
SSR2
ADAM15
Position on chr1 (Mb)

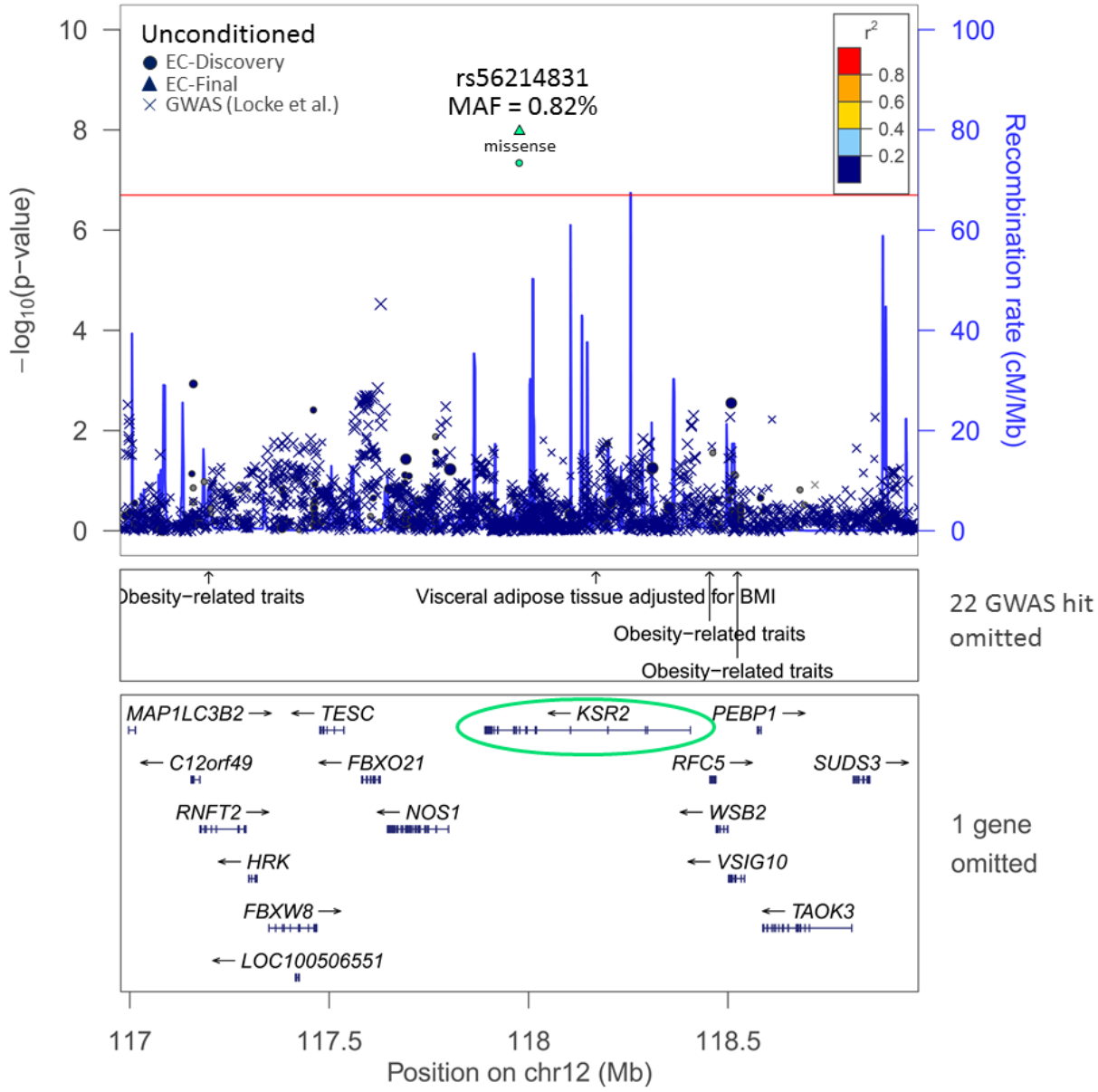
RAPGEF3 - All-ancestries sex-combined additive



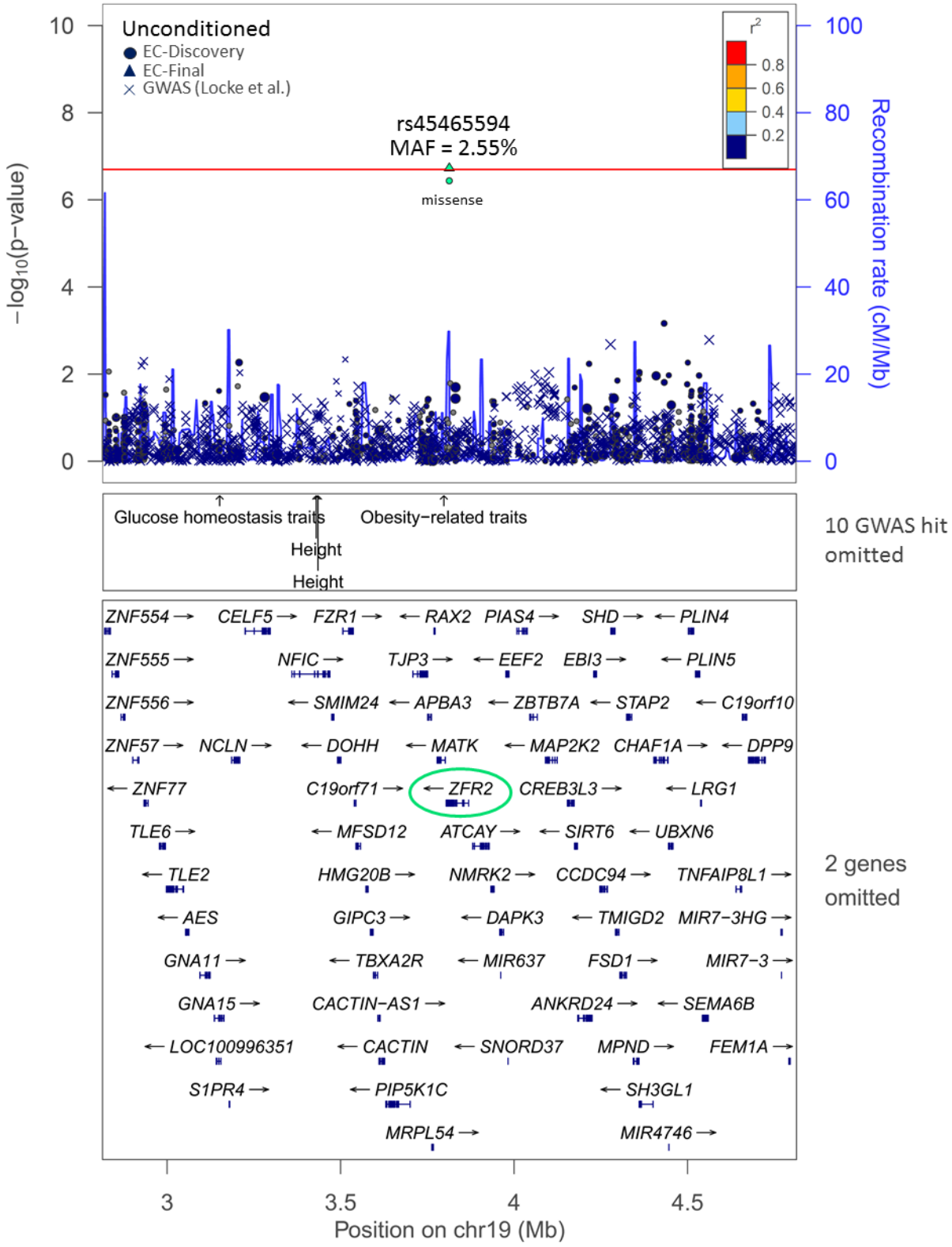
RAB21 - All-ancestries sex-combined additive



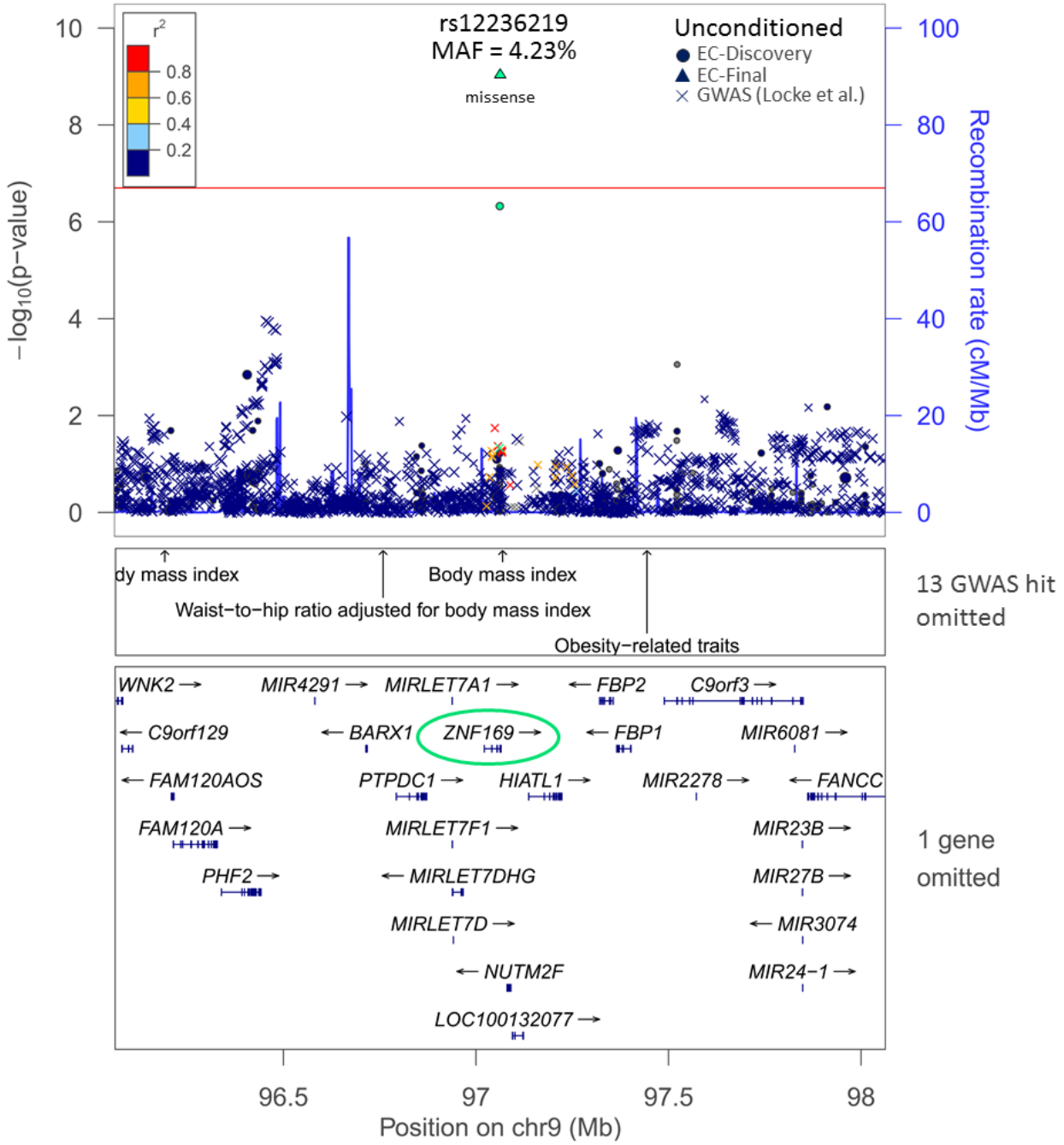
KSR2 - All-ancestries sex-combined additive



ZFR2 - All-ancestries women additive

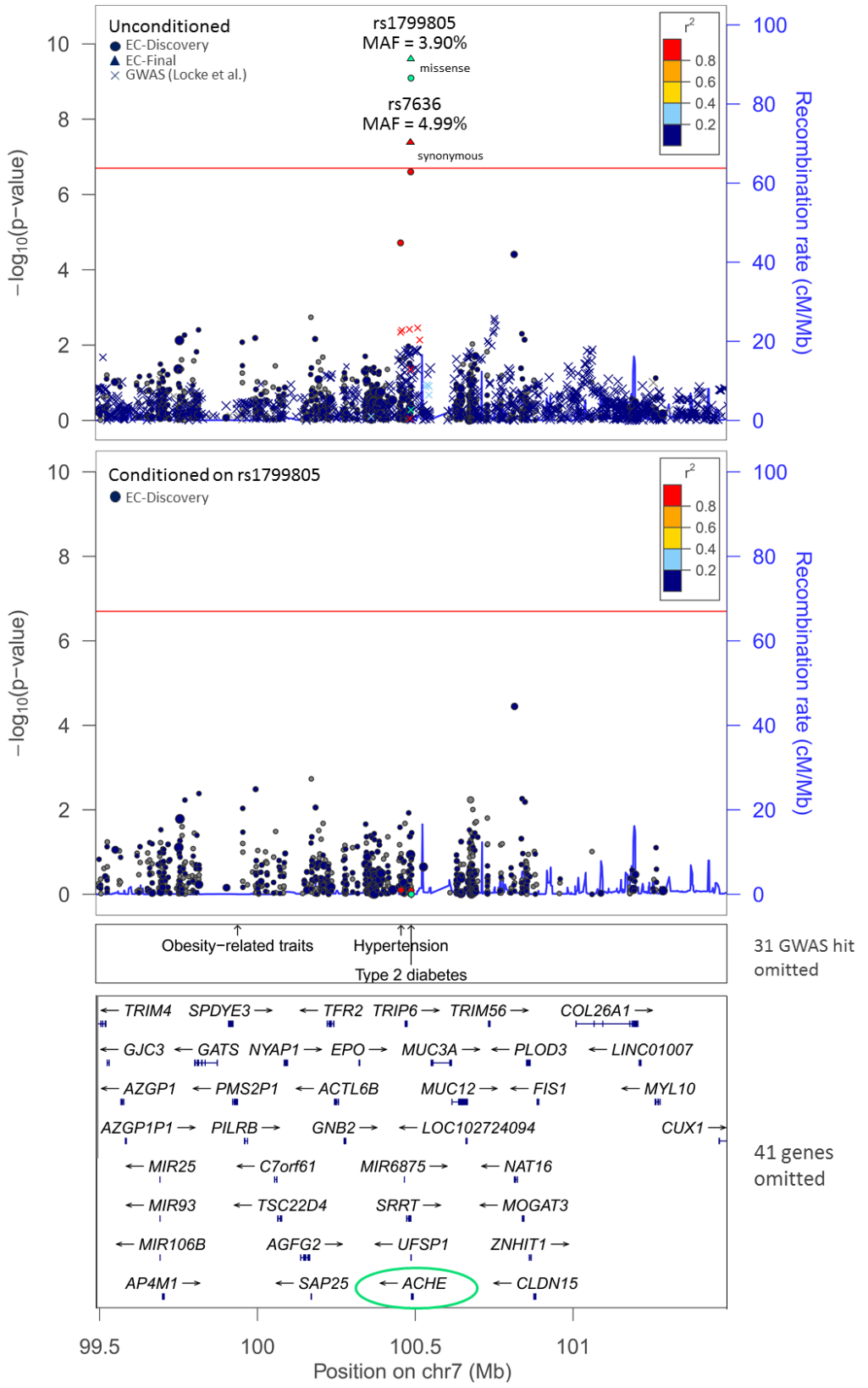


ZNF169 - Europeans sex-combined additive

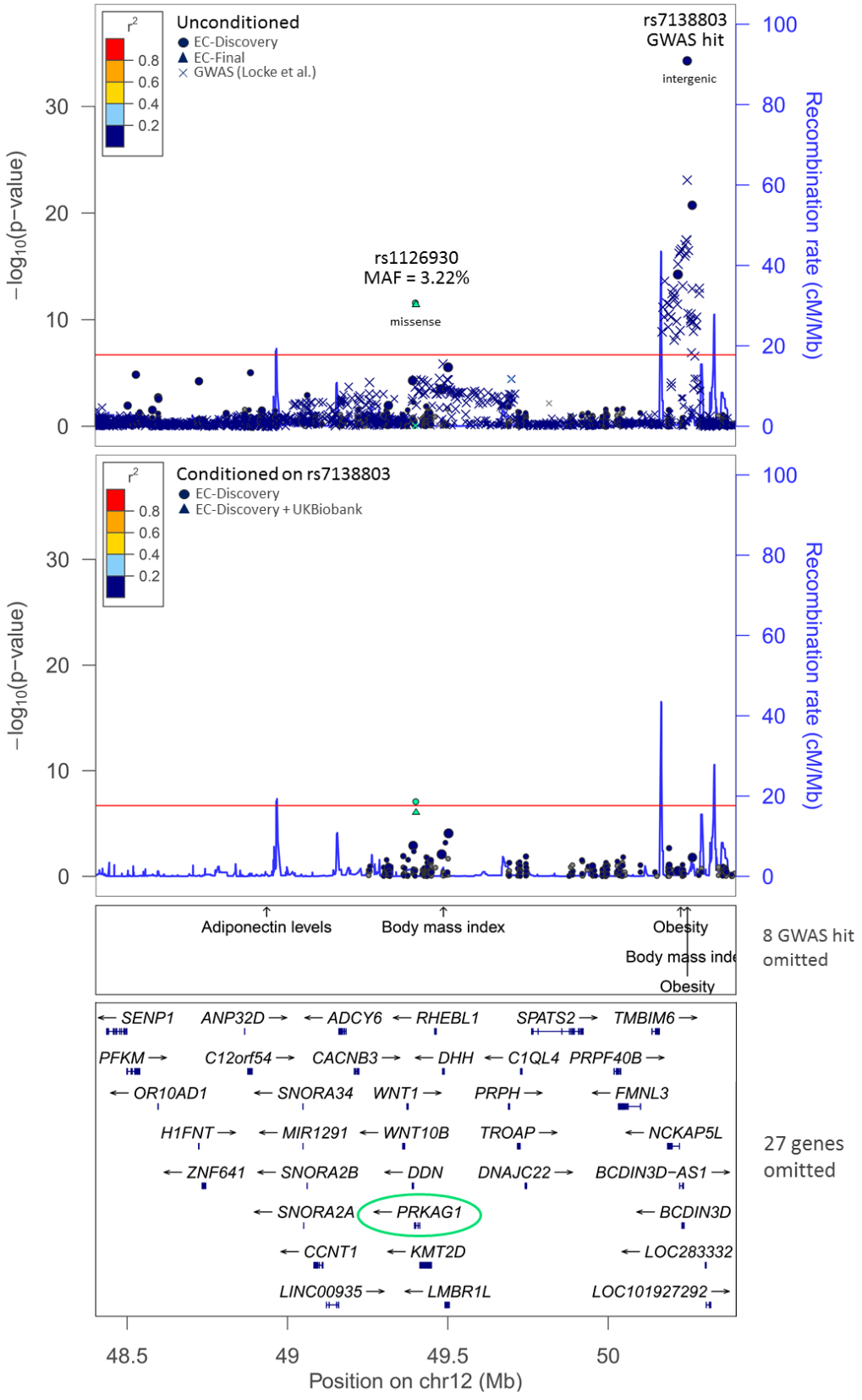


B

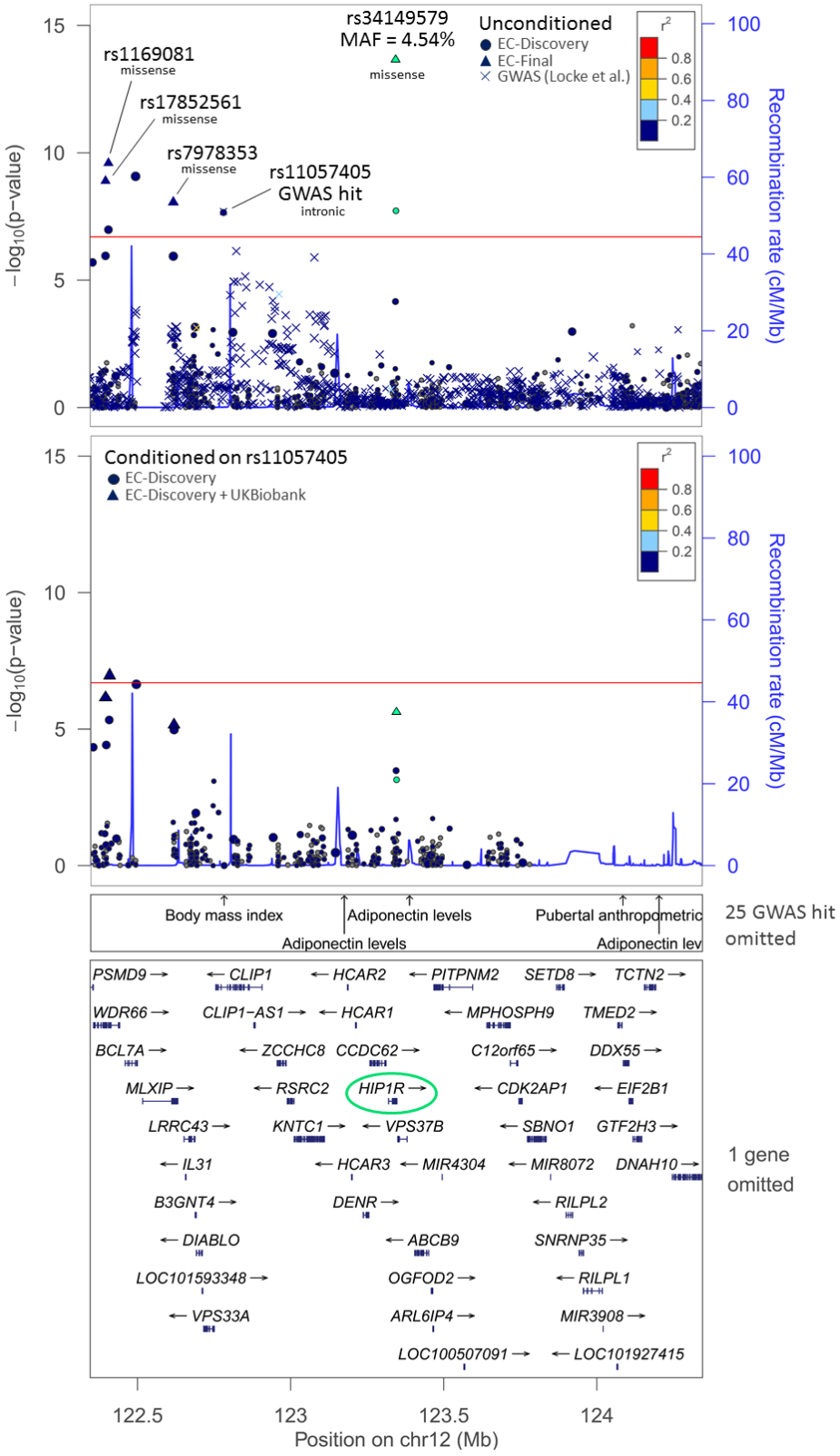
ACHE - All-ancestries sex-combined additive



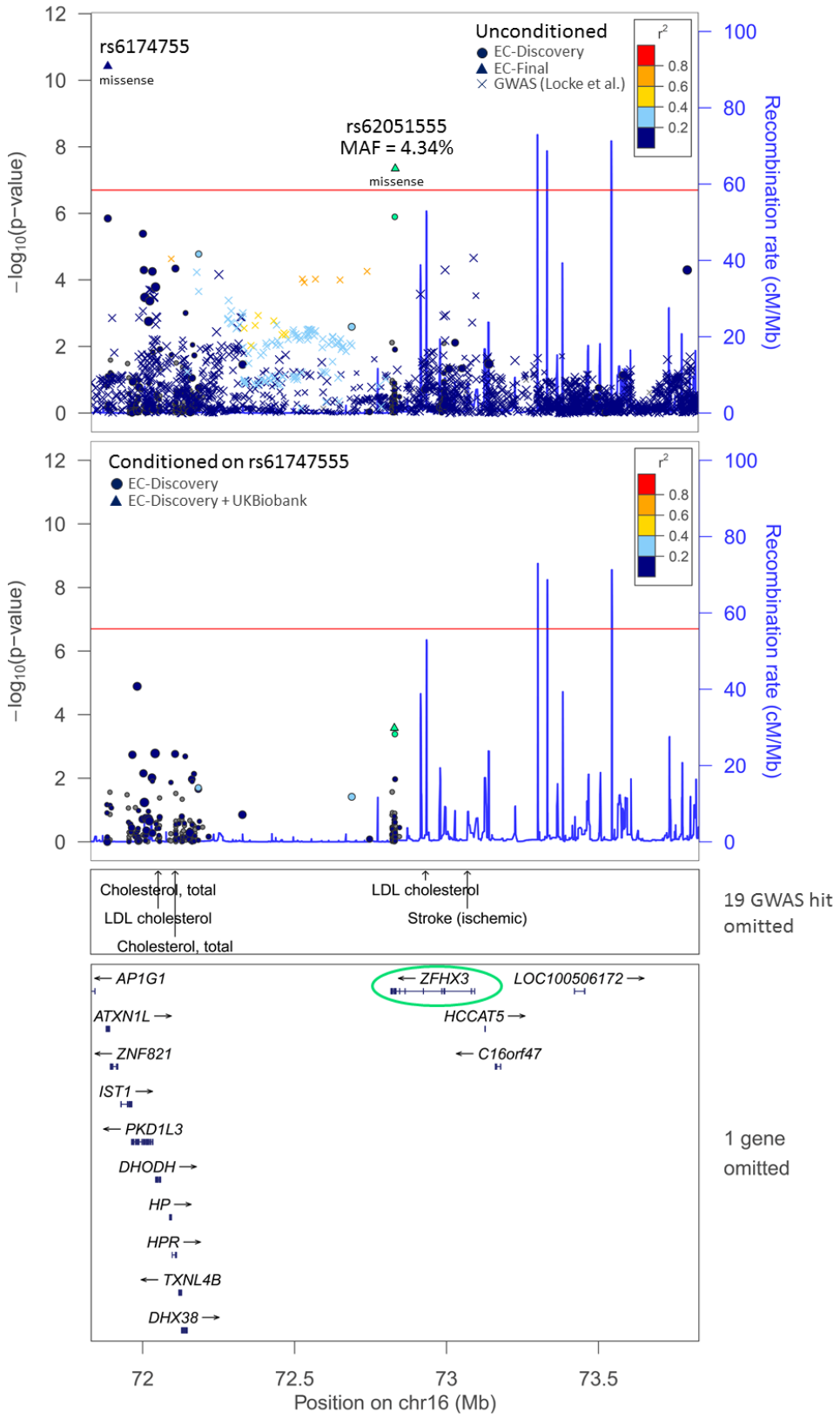
PRKAG1 - All-ancestries sex-combined additive



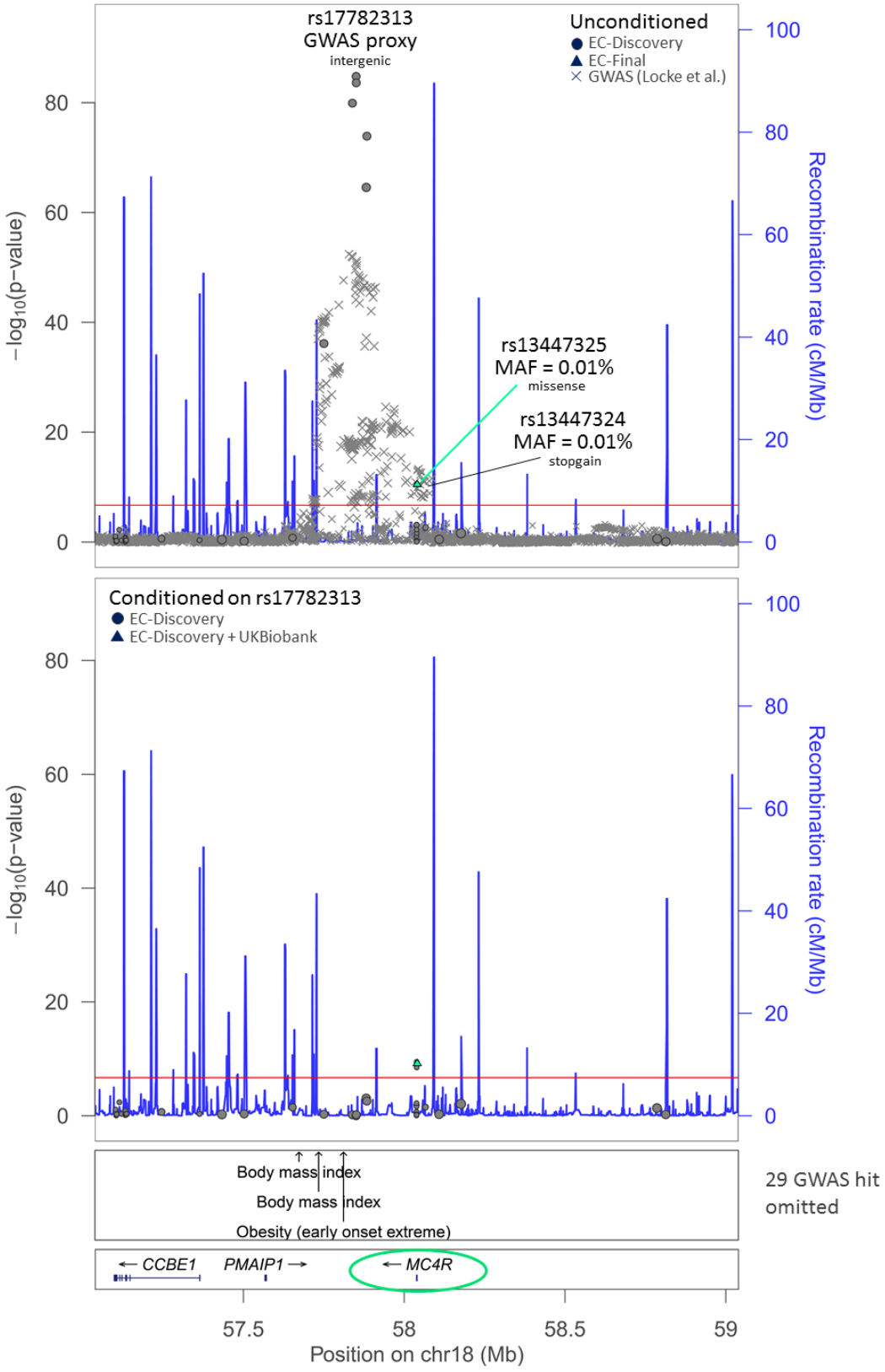
HIP1R - All-ancestries sex-combined additive



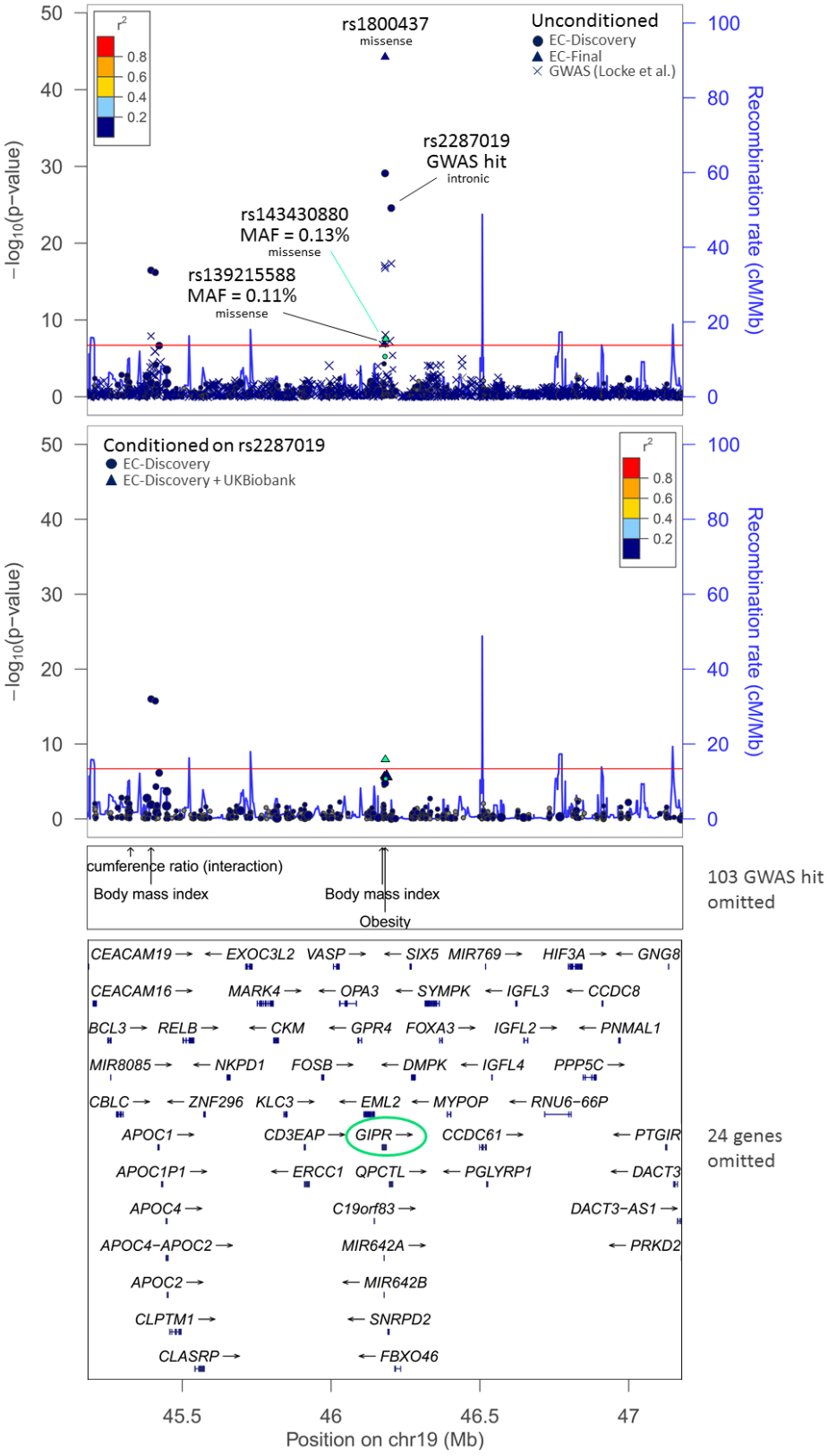
ZFHX3 - All-ancestries sex-combined additive



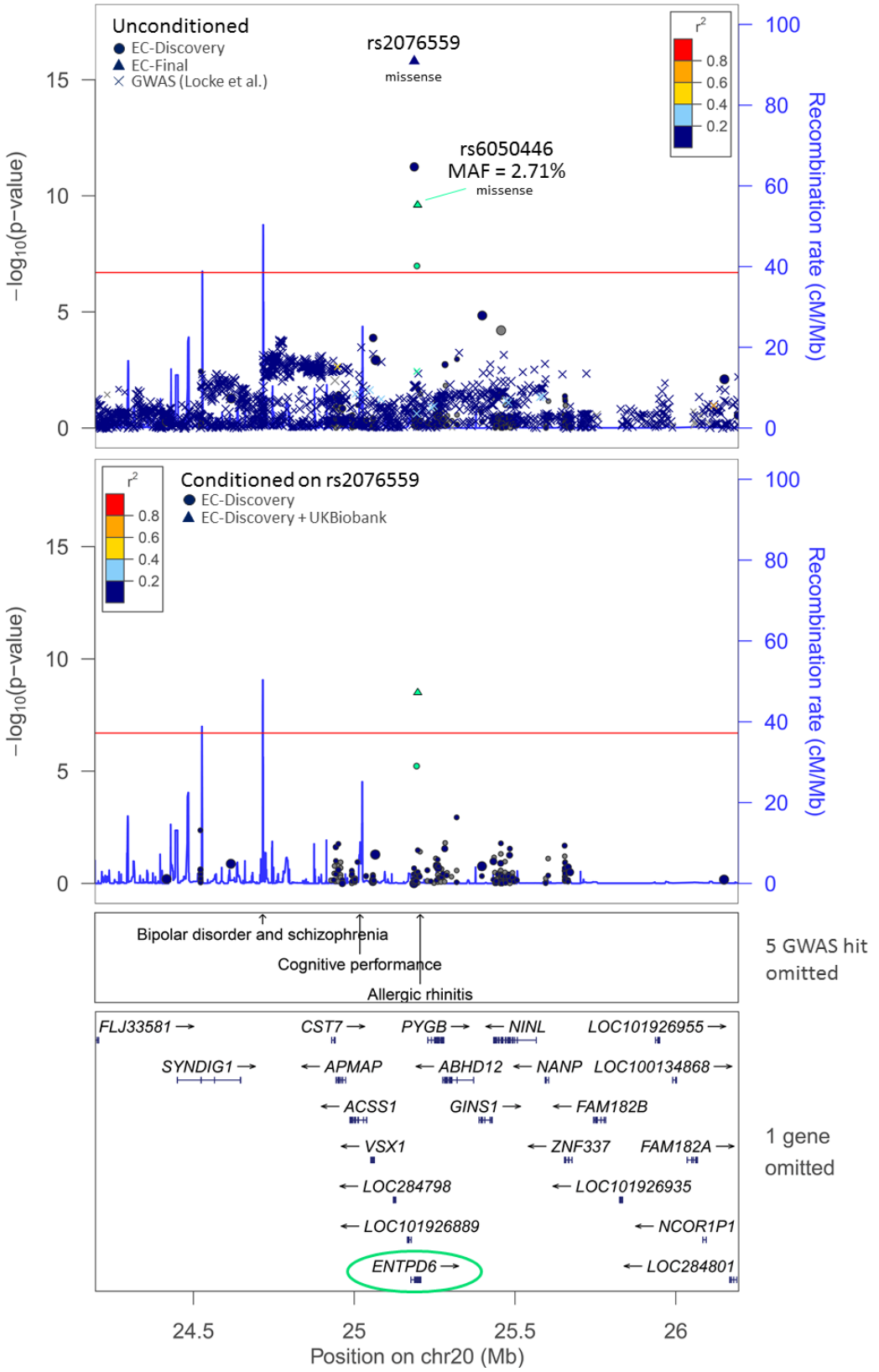
MC4R - All-ancestries sex-combined additive



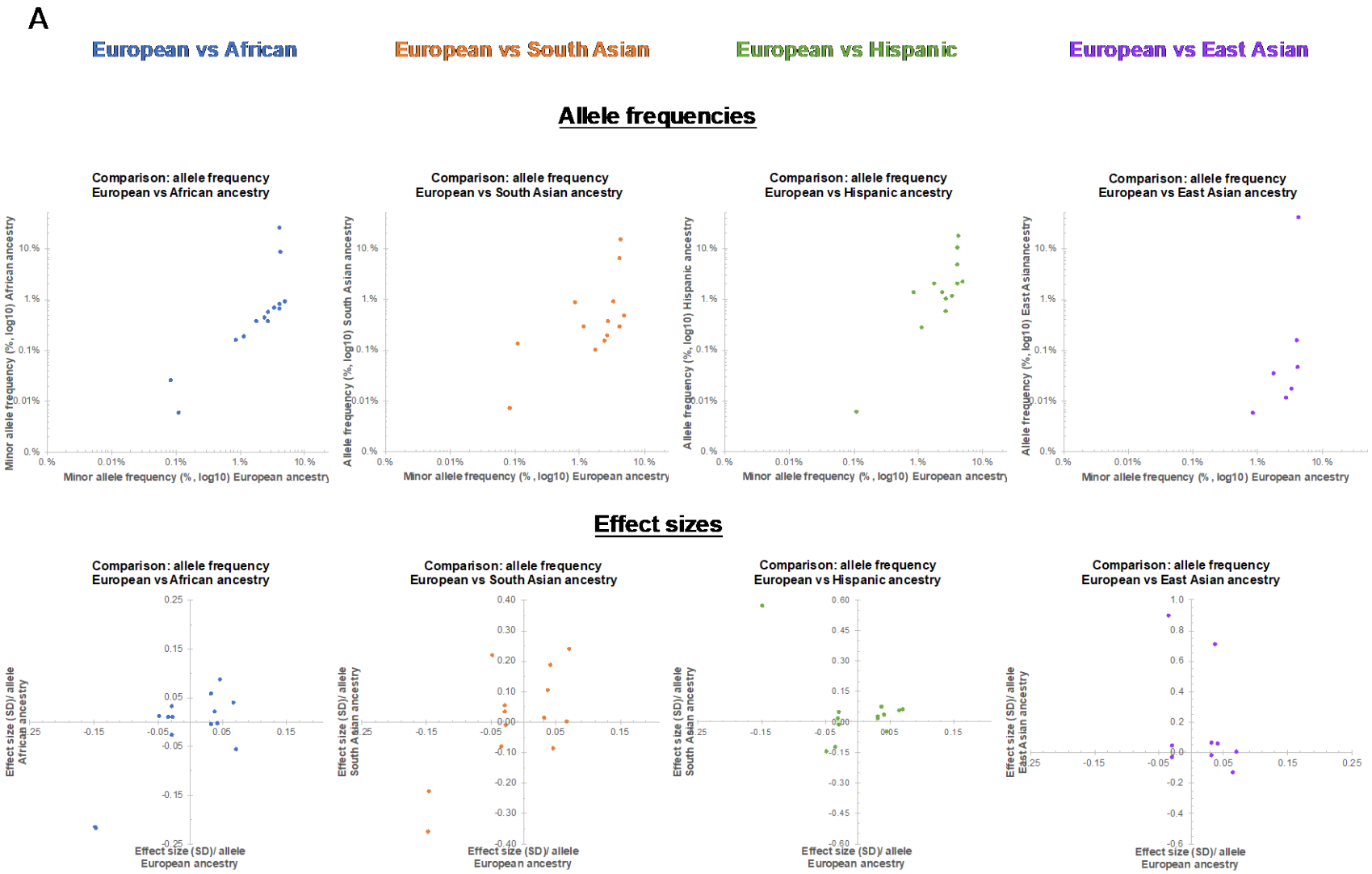
GIPR - All-ancestries sex-combined additive



ENTPD6 - All-ancestries sex-combined additive



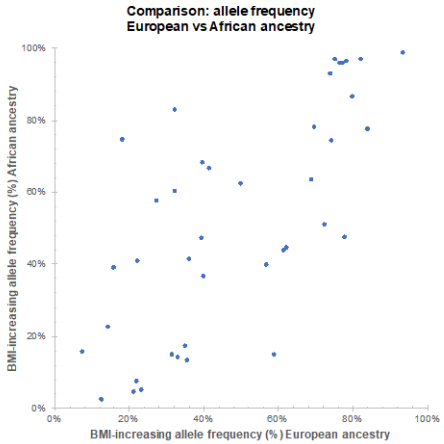
Supplementary Figure 6 | Relationship of allele frequencies and effect sizes of novel SNVs between European-ancestry and other ancestry populations (see also Supplementary Table 7). Panel A shows the data for the minor alleles of 14 low-frequency and rare SNVs. Panel B shows the data for the BMI-increasing allele of the 41 common SNVs.

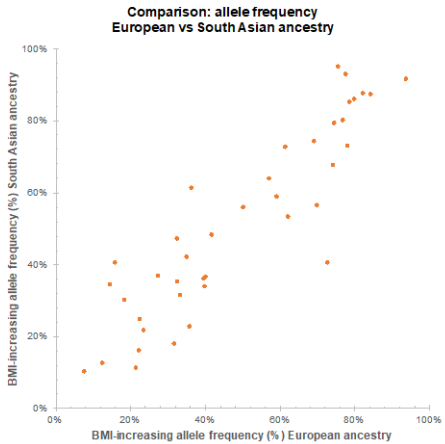


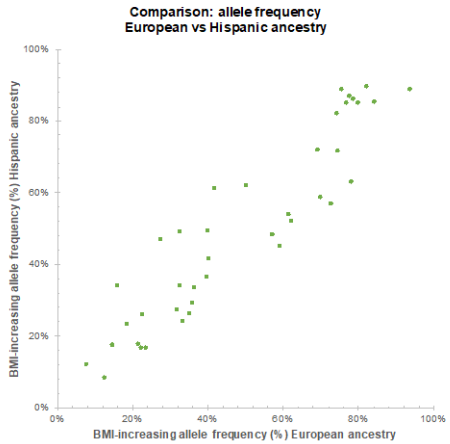
B

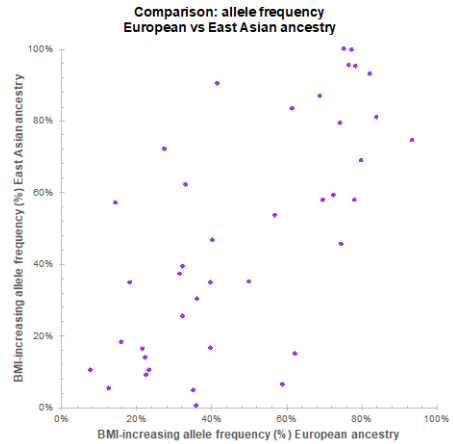
European vs African | European vs South Asian | European vs Hispanic | European vs East Asian

Allele frequencies

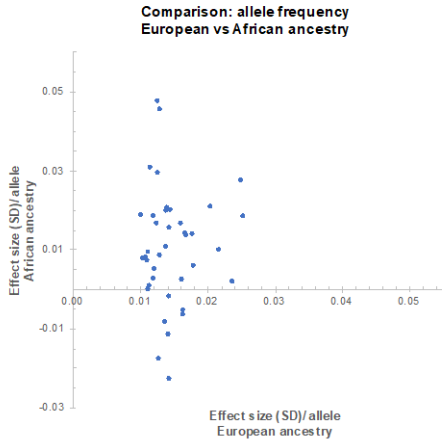


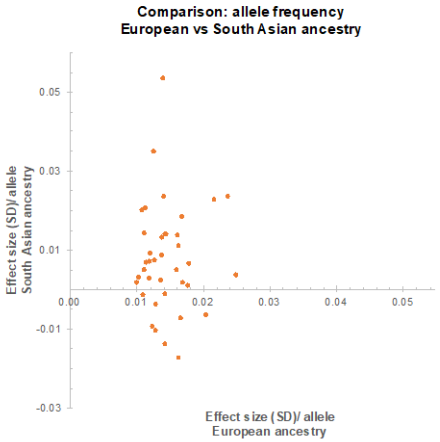


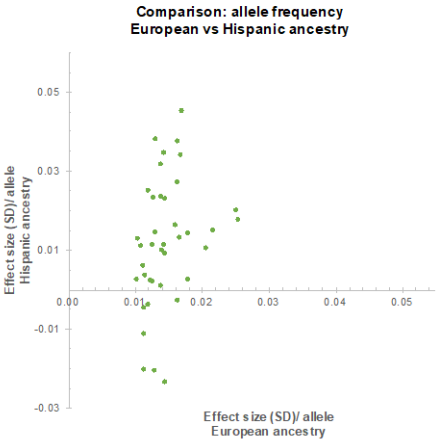


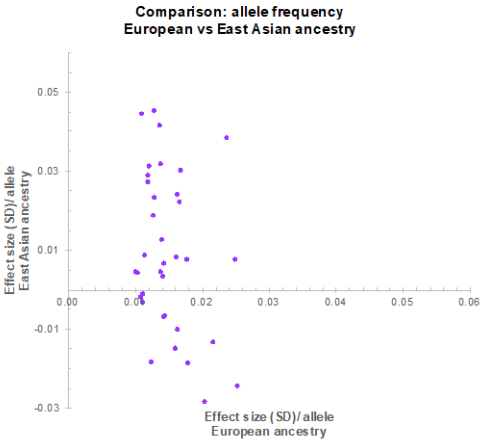


Effect sizes

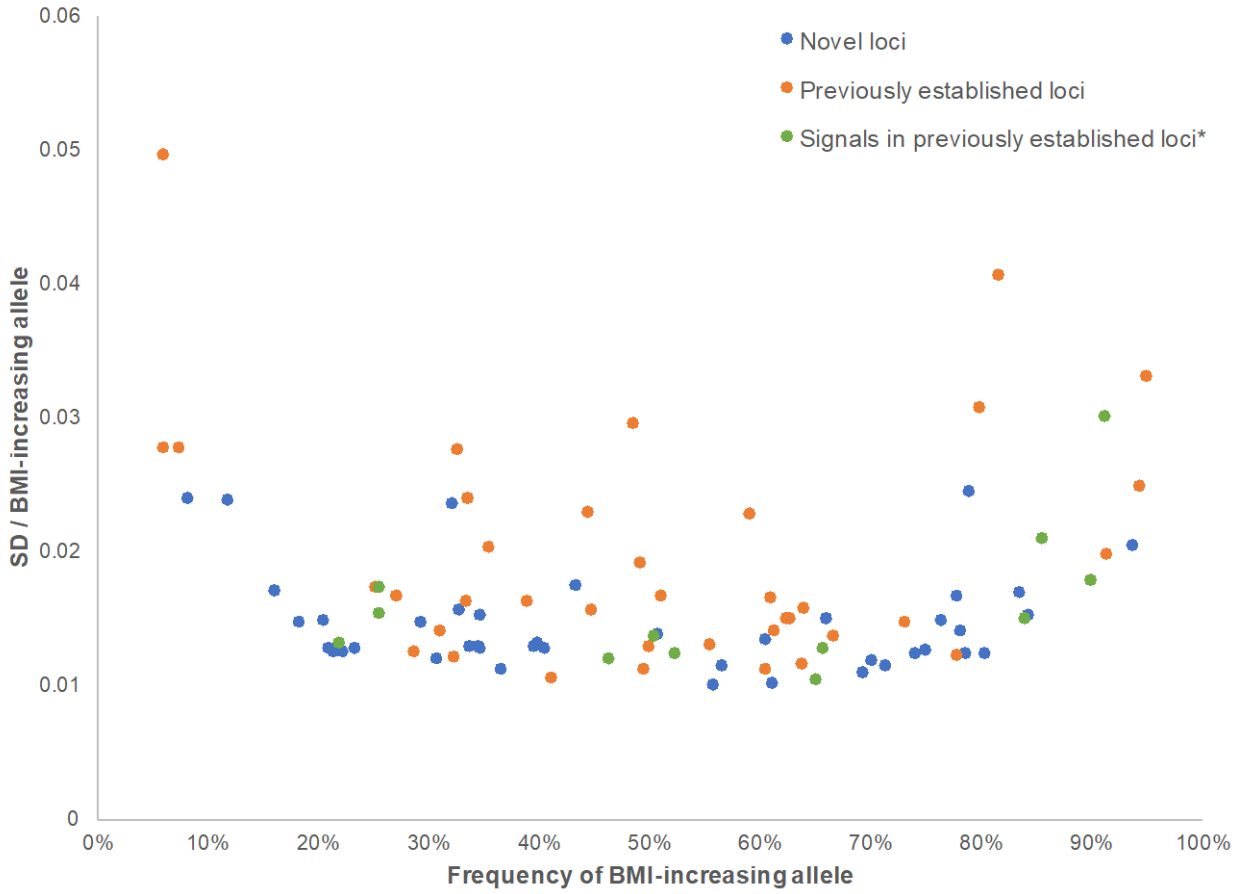




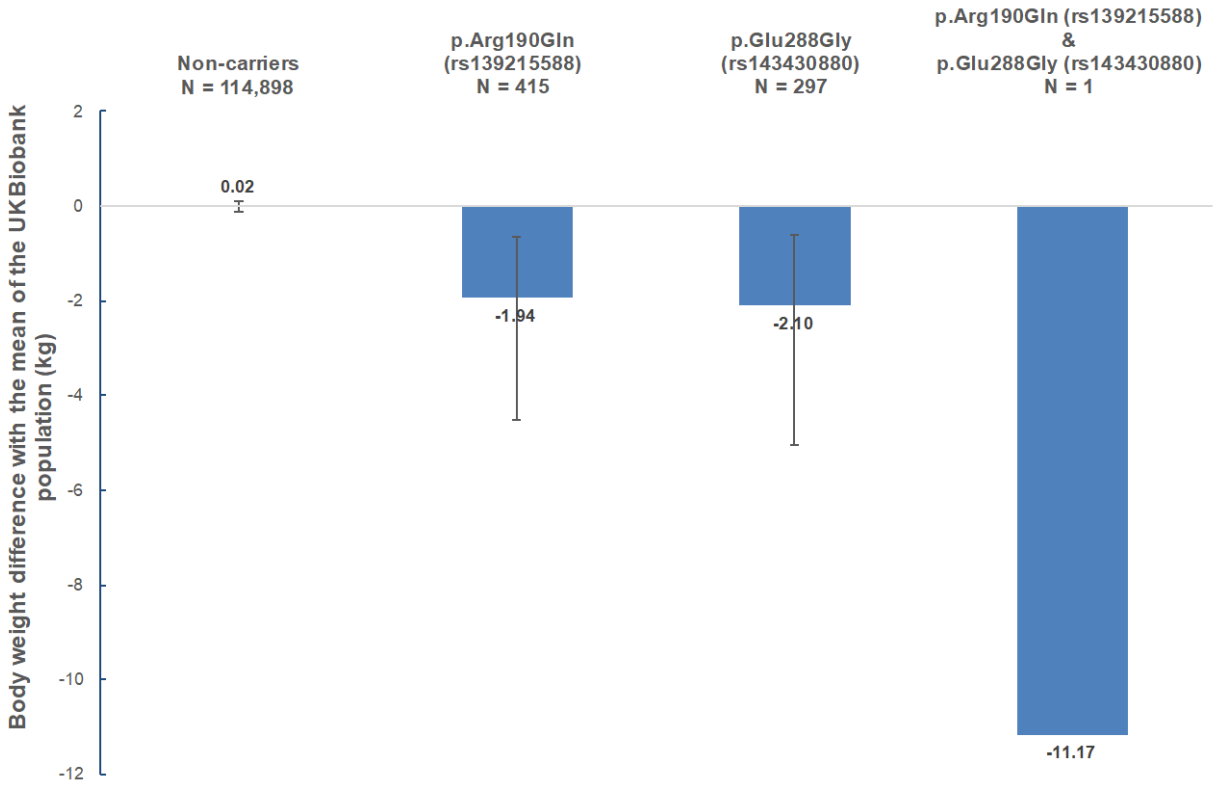




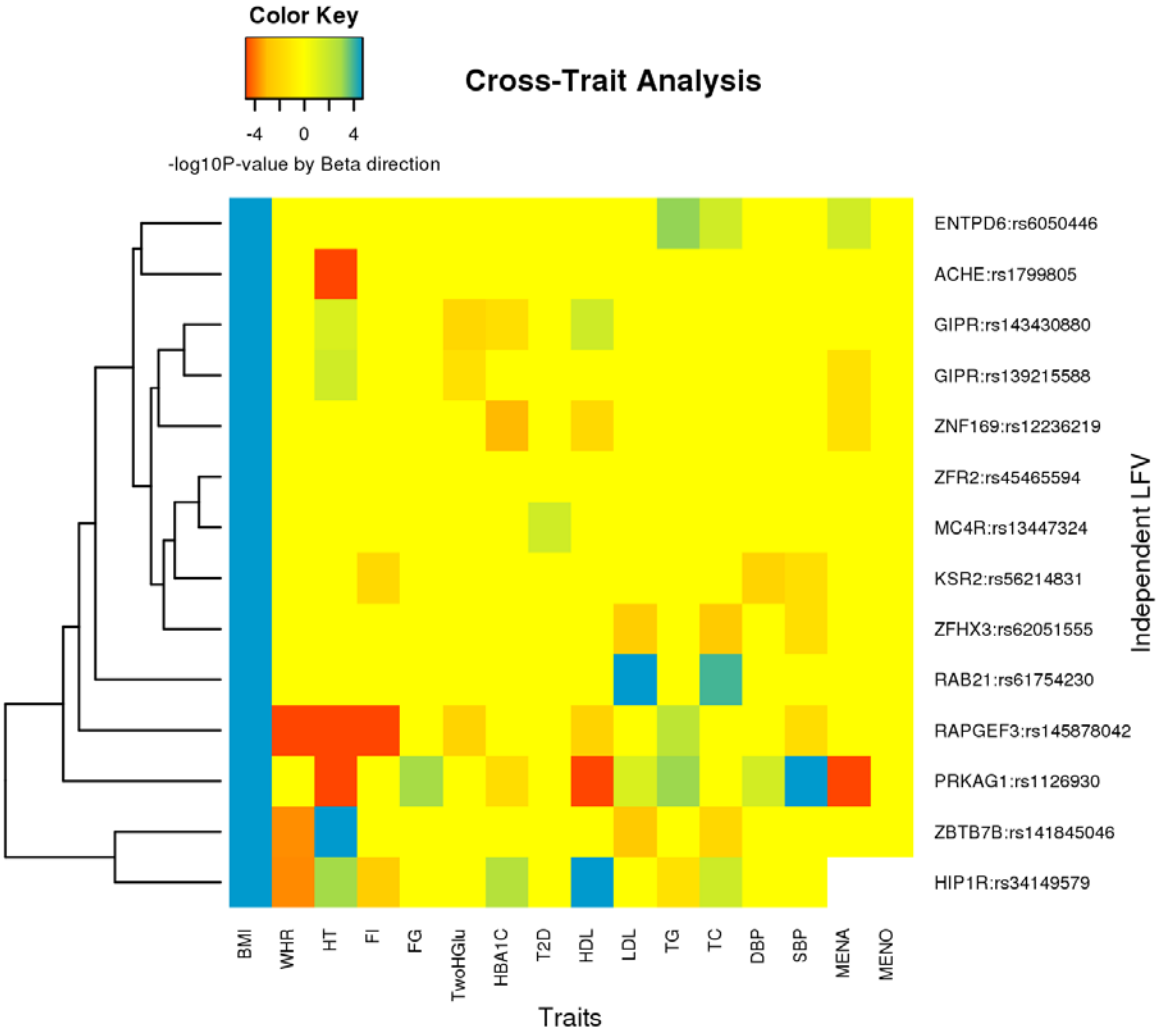
Supplementary Figure 7 | Effect sizes (y-axis) of the 92 common coding variants by their BMI-increasing allele frequency. Effect sizes are expressed in SD per allele (**Supplementary Table 4**). Blue dots represent the 42 novel loci, orange dots represent loci that have been identified before in GWAS for obesity traits, and green dots represent association signals in previously established loci, but for which conditional analyses was not able to convincingly determine the signal as secondary or not (i.e. the previously established lead SNP was not available on the chip).



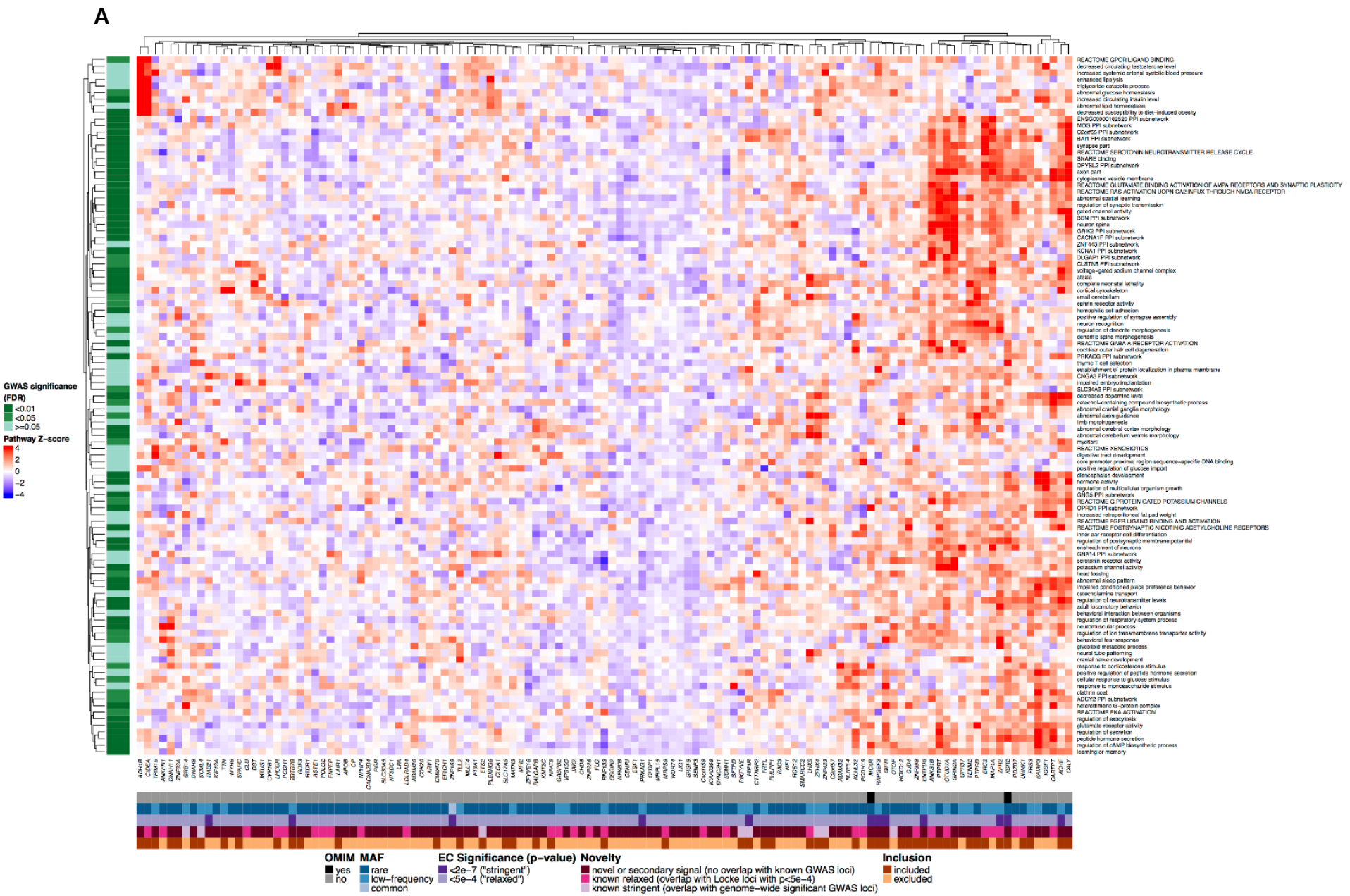
Supplementary Figure 8 | Effects of the two rare SNVs (p.Arg190Gln, p.Glu288Gly) in *GIPR* on BMI in the UK Biobank (N = 115,611, Interim release). Y-axis shows the difference from mean BMI in the UKBiobank, after adjusting for age and sex.

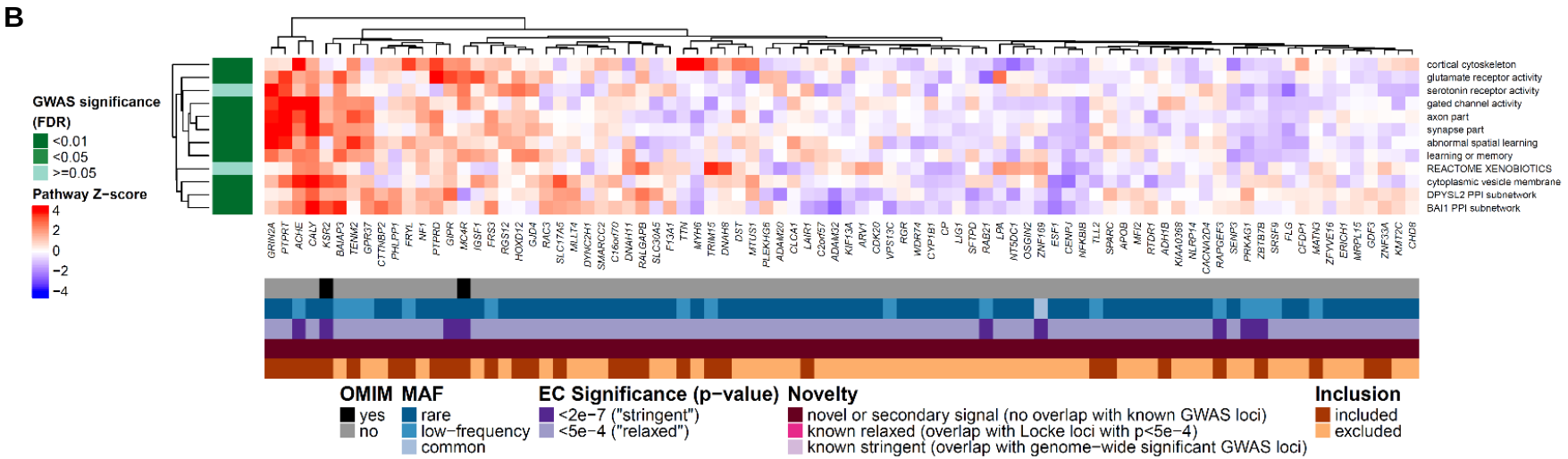


Supplementary Figure 9 | Heatmaps of cross-trait associations for the novel R/LF independent loci identified in the final combined meta-analysis. Heatmap squares are –log10(*P*-values) with red-to-blue shading based on beta effect direction for the BMI-increasing allele in the final combined meta-analysis (blue). Green-to-blue shading hits correspond to positive beta effects with *P*-values between 0.05 and <2E-5, orange-to-red shading hits correspond to negative beta effects with *P*-values between 0.05 to <2E-5, yellow squares are not significant (*P*>0.05), and white squares are missing values. Clustering was done using the complete linkage method with Euclidean distance measure for the loci. SNVs clustering together are more significantly associated with the same set of traits.



Supplementary Figure 10 | Heatmaps showing full DEPICT gene set enrichment results A) of rare and low frequency nonsynonymous SNVs (from main text figure 2), B) of novel rare and low frequency nonsynonymous SNVs, and C) nonsynonymous SNVs of all allele frequencies. For any given square, the color indicates how strongly the corresponding gene (shown on the x-axis) is predicted to belong to the reconstituted gene set (y-axis). This value is based on the gene's z-score for gene set inclusion in DEPICT's reconstituted gene sets, where red indicates a higher and blue a lower z-score. To visually reduce redundancy and increase clarity, we chose one representative "meta-gene set" for each group of highly correlated gene sets based on affinity propagation clustering (**Online Methods, Supplementary Information**). Heatmap intensity and DEPICT *P*-values (see *P*-values in **Supplementary Tables 17-19**) correspond to the most significantly enriched gene set within the meta-gene set. Annotations for the genes indicate (1) whether the gene has an OMIM annotation as underlying a monogenic obesity disorder (black and grey), (2) the minor allele frequency of the significant ExomeChip (EC) variant (shades of blue; if multiple variants, the lowest-frequency variant was kept), (3) whether the variant's *P*-value reached array-wide significance (<2x10-7) or suggestive significance ($<5x10^{-4}$) (shades of purple), (4) whether the variant was novel, overlapping "relaxed" GWAS signals from Locke et al.[3] (GWAS $P<5x10^{-4}$), or overlapping "stringent" GWAS signals (GWAS $P<5x10^{-8}$) (shades of pink), and (5) whether the gene was included in the gene set enrichment analysis or excluded by filters (shades of brown/orange) (**Online Methods and Supplementary Information**). Annotations for the gene sets indicate if the meta-gene set was found significant (shades of green; FDR <0.01, <0.05, or not significant) in the DEPICT analysis of GWAS results from Locke et al.[3]


A
GWAS significance (FDR)
<0.01
<0.05
>=0.05
Pathway Z-score
4
2
0
−2
−4
REACTOME GPCR LIGAND BINDING
decreased circulating testosterone level
increased systemic arterial systolic blood pressure
enhanced lipolysis
triglyceride catabolic process
abnormal glucose homeostasis
increased circulating insulin level
abnormal lipid homeostasis
decreased susceptibility to diet−induced obesity
ENSG00000182520 PPI subnetwork
MOG PPI subnetwork
C9orf85 PPI subnetwork
BAI1 PPI subnetwork
synapse part
REACTOME SEROTONIN NEUROTRANSMITTER RELEASE CYCLE
SNARE binding
DPYSL2 PPI subnetwork
axon part
cytoplasmic vesicle membrane
REACTOME GLUTAMATE BINDING ACTIVATION OF AMPA RECEPTORS AND SYNAPTIC PLASTICITY
REACTOME PAS ACTIVATION UOPN CA2 INFUX THROUGH NMDA RECEPTOR
abnormal spatial learning
regulation of synaptic transmission
gated channel activity
BSN PPI subnetwork
neuron spine
GRIK2 PPI subnetwork
CACNA1F PPI subnetwork
ZNF143 PPI subnetwork
KCNA1 PPI subnetwork
OLGAP1 PPI subnetwork
CLSTN3 PPI subnetwork
voltage−gated sodium channel complex
ataxia
complete neonatal lethality
cortical cytoskeleton
small cerebellum
ephrin receptor activity
homophilic cell adhesion
positive regulation of synapse assembly
neuron recognition
regulation of dendrite morphogenesis
dendritic spine morphogenesis
REACTOME GABA A RECEPTOR ACTIVATION
cochlear outer hair cell degeneration
PRKACG PPI subnetwork
thymic T cell selection
establishment of protein localization in plasma membrane
CNGA3 PPI subnetwork
impaired embryo implantation
SLC34A3 PPI subnetwork
decreased dopamine level
catechol−containing compound biosynthetic process
abnormal cranial ganglia morphology
abnormal axon guidance
limb morphogenesis
abnormal cerebral cortex morphology
abnormal cerebellum vermis morphology
myotonia
REACTOME XENOBIOTICS
digestive tract development
core promoter proximal region sequence−specific DNA binding
positive regulation of glucose import
diencephalon development
hormone activity
regulation of multicellular organism growth
GNGS PPI subnetwork
REACTOME G PROTEIN GATED POTASSIUM CHANNELS
OPRD1 PPI subnetwork
increased retroperitoneal fat pad weight
REACTOME FGFR LIGAND BINDING AND ACTIVATION
REACTOME POSTSYNAPTIC NICOTINIC ACETYLCHOLINE RECEPTORS
inner ear receptor cell differentiation
regulation of postsynaptic membrane potential
ensheathment of neurons
GNA14 PPI subnetwork
serotonin receptor activity
potassium channel activity
head tossing
abnormal sleep pattern
impaired conditioned place preference behavior
catecholamine transport
regulation of neurotransmitter levels
adult locomotory behavior
behavioral interaction between organisms
regulation of respiratory system process
neuromuscular process
regulation of ion transmembrane transporter activity
behavioral fear response
glycolytic metabolic process
neural tube patterning
cranial nerve development
response to corticosterone stimulus
positive regulation of peptide hormone secretion
cellular response to glucose stimulus
response to monosaccharide stimulus
clathrin coat
ADCY2 PPI subnetwork
heterotrimeric G−protein complex
REACTOME PKA ACTIVATION
regulation of exocytosis
glutamate receptor activity
regulation of secretion
peptide hormone secretion
regulation of cAMP biosynthetic process
learning or memory
ADH1B CYP2E1 TSHR AKAP11 ZNF638 GNAI1 DNAH8 SOBP4 RABS1 KCNT2 ITIH MYH6 SPARC CLU DST MTUS1 CYP7B1 LRCH3 RYR3 ZBTB7B GDF3 RTDR1 ACTC1 PKD2 ENPEP LAIR1 APOB CPO NPHP4 CACNA2D4 RGR SLC30A5 NTSC1 LPL LOUNAD4 ADAM33 CDKS2 ARV1 C16orf70 ENOX1 ZNF532 TLL2 MLL4 P3A1 ITGB2 PLEKHA6 CLCA1 SLC17A6 MAP3 NOS2 ZFYVE16 RALGAPB KMT2C MYO1E GABRB2 VPS13C JAK2 CA13 ZNF98 FLG RNF133 OSGIN2 NOS1AP CEMP1 ESF1 PRKAG1 CYCS MRPL15 MRPS9 WDR74 LAT1 SSH3 SENP3 C1orf59 KIAA0368 RNF207 SCMH1 SFTPD PNKTVE HMGB3 CTTNBP2 FPPL PALLPH HAO1 NOL RGS12 SMARCC2 LHX3 ZNF404 C2orf57 ZNF483 ADAM32 MYO5A KLHL32 PCDH15 MC4R RANGEF3 OTOF HOXD13 GJD4 ZNF365 FAT1B KANK1B ITPRIT ZDHHC7 GPR37 TENM2 PTPRO EPS8 MAP1A ZFR2 KSR2 PTPRZ1 UNKK1 FRS3 BAAP3 KIF1B CNTNAP1 ACHE CALY
OMIM
yes
no
MAF
rare
low−frequency
common
EC Significance (p−value)
<2e−7 ("stringent")
<5e−4 ("relaxed")
Novelty
novel or secondary signal (no overlap with known GWAS loci)
known relaxed (overlap with Locke loci with p<5e−4)
known stringent (overlap with genome−wide significant GWAS loci)
Inclusion
included
excluded


B
GWAS significance (FDR)
<0.01
<0.05
>=0.05
Pathway Z-score
4
2
0
−2
−4
cortical cytoskeleton
glutamate receptor activity
serotonin receptor activity
gated channel activity
axon part
synapse part
abnormal spatial learning
learning or memory
REACTOME XENOBIOTICS
cytoplasmic vesicle membrane
DPYSL2 PPI subnetwork
BAI1 PPI subnetwork
GRIN2A PTPRT ACHE CALY KSR2 BAIAP3 TENM2 GPR37 CTTNBP2 PHLPP1 FRYL NF1 PTPRD GIPR MC4R IGSF1 FRS3 RGS12 HOXD12 GJD4 RAC3 SLC17A5 MLLT4 DYNC2H1 SMARCC2 C16orf70 DNAH11 RALGAPB SLC30A5 F13A1 TTN MYH6 TRIM15 DNAH8 DST MTUS1 PLEKHG6 ADAM20 CLCA1 LAIR1 C2orf57 ADAM32 KIF13A ARV1 CDK20 VPS13C RGR WDR74 CYP1B1 CP LIG1 SFTPD RAB21 LPA NT5DC1 OSGIN2 ZNF169 ESF1 CENPJ NFKBIB TLL2 SPARC APOB MFI2 RTDR1 ADH1B KIAA0368 NLRP14 CACNA2D4 RAPGEF3 SENP3 PRKAG1 ZBTB7B SRSF9 FLG CFDP1 MATN3 ZFYVE16 ERICH1 MRPL15 GDF3 ZNF33A KMT2C CHD8
OMIM MAF
yes
no
rare
low−frequency
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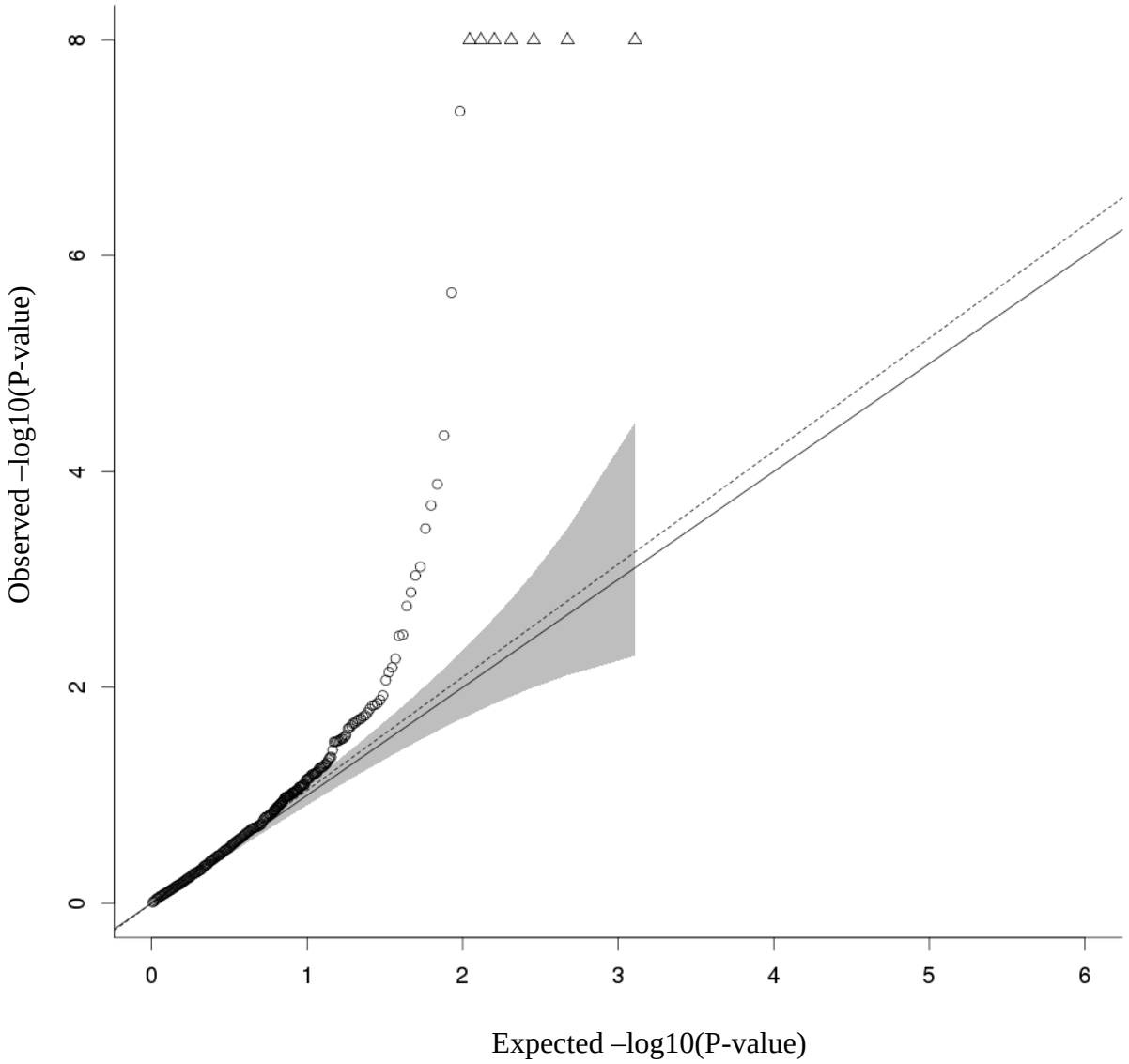
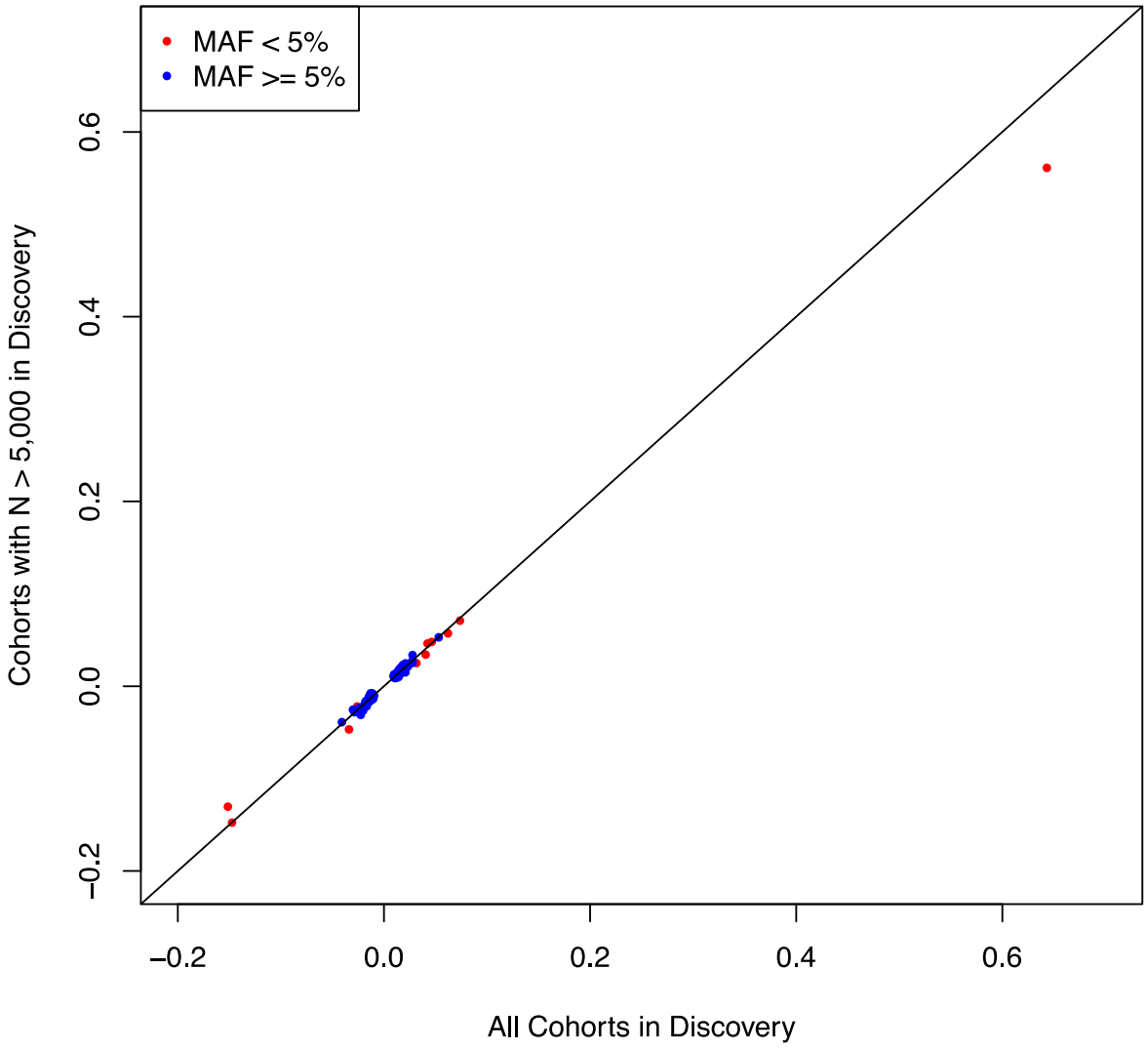
EC Significance (p−value)
<2e−7 ("stringent")
<5e−4 ("relaxed")
Novelty
novel or secondary signal (no overlap with known GWAS loci)
known relaxed (overlap with Locke loci with p<5e−4)
known stringent (overlap with genome−wide significant GWAS loci)
Inclusion
included
excluded
C

Supplementary Figure 11 | Quantile-quantile plot for BMI associations for rare and low-frequency coding SNVs located in monogenic and syndromic genes of obesity. Single variant association results obtained in the final combined meta-analysis are enriched for coding SNVs located in monogenic and syndromic genes of obesity (see gene list and results in **Supplementary Table 21**).



Supplementary Figure 12 | Scatter plot comparison of the effect sizes for all variants that reached significance in the European-ancestry-discovery results (n = 526,508) and results including only studies with sample sizes of more than 5,000 individuals (n = 317,511).

5.



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